

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: May 27, 2004, 05:54:07 ; Search time 20 Seconds
(without alignments)
1519.826 Million cell updates/sec

Title: US-09-403-882A-2
Perfect score: 1622
Sequence: 1 MAEVLQESGGGLVQPGSR.....VLTITSLIILMLWQKKPR 316
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78.*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	892.5	55.0	268	A56446	Ig heavy chain V r
2	718.5	44.3	249	S41374	single chain Fv an
3	626.5	38.6	233	JC5322	p53 specific singl
4	555.5	34.2	213	S68213	Ig heavy chain (Ma
5	535	33.0	136	G1MS21	Ig heavy chain pre
6	522.5	32.2	121	B34871	Ig heavy chain V r
7	516	31.8	130	1JL0079	Ig kappa chain pre
8	514	31.7	235	S25058	Ig kappa chain - m
9	511	31.5	107	A30562	Ig kappa chain V r
10	508	31.3	103	S29591	Ig kappa chain V r
11	508	31.3	104	B49049	Ig kappa chain V r
12	506	31.2	106	F50071	Ig kappa chain V r
13	506	31.2	107	B30562	Ig kappa chain V r
14	501	30.9	107	S11118	Ig kappa chain V r
15	498	30.7	107	PC4405	Ig kappa chain V r
16	498	30.7	107	S11119	Ig kappa chain V r
17	490	30.2	107	S11121	Ig kappa chain V r
18	488	30.1	107	PT0406	Ig kappa chain V r
19	484.5	29.9	143	S23624	Ig heavy chain V r
20	483	29.8	107	S11117	Ig kappa chain V r
21	482	29.7	120	S12953	Ig kappa chain V r
22	481.5	29.7	108	G30560	Ig kappa chain V r
23	480	29.6	94	D25913	Ig heavy chain V r
24	479	29.5	100	S29590	Ig kappa chain V r
25	478	29.5	107	S11112	Ig kappa chain V r
26	478	29.5	108	PD0015	Ig heavy chain V r
27	476	29.3	107	FH0011	Ig kappa chain V r
28	473	29.2	97	PH1084	Ig light chain V r
29	473	29.2	114	S46392	Ig heavy chain V r

ALIGNMENTS

RESULT 1

A56446
Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)
C:Species: Mus musculus (house mouse)
C>Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996
C:Accession: A56446
R:Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.
J. Biol. Chem. 270, 7829-7835, 1995
A:Title: A high affinity digoxin-binding protein displayed on M13 is functionally identical
A:Reference number: A56446; MUID:95229583; PMID:7713873
A:Accession: A56446
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-268 <TAN>
A:Cross-references: GB:U20617
C:Keywords: heterotetramer; immunoglobulin

Query Match 55.0%; Score 892.5; DB 2; Length 268;
Best Local Similarity 65.9%; Pred. No. 2.7e-52;
Matches 176; Conservative 26; Mismatches 52; Indels 13; Gaps 2;

QY 1 MAEVLQESGGGLVQPGSRKLSCAASGFTFSFGMHVVRQAPKGLWVAIYSSGSETI 60
DB 1 MAQVKLQESGAELVKPGASVKLSCTTSQGNFKDTYMHVKQRPQGLEWIGRIAPANGIT 60
QY 61 YYADTVKGRFTISRDNPKNTLFLQWTSLSRSDTYNYCA---RDYGYWGGTIVTVSS 116
DB 61 KYDPKFGKATIAADTSSNTAYLQLSLTSDTAVYCYSLTRYENWGGTIVTVSS 120
QY 117 GGGGGGGGGGGGGSDIELTQSPAIMASPGERTVMTCSASSVRYMNFQKSGTSPKR 176
DB 121 GGGGGGGGGGGGGSDIELTQSPAIMASLGEKVTMSCRASSVNFYVYQKSDASPKL 180
QY 177 WYDTKLSGGVPAFPFGSGSGTYSVLTSSMEADATYTCQWSSNPLTFGAGTKLEL 236
DB 181 WYTYTSLPFGVPAFPFGSGSGSNYSVLTSSMEGEDATYTCQOFTSPFTFGSGTKLEI 240
QY 237 KKA-----AAEKLISEEDLNGA 254
DB 241 KSAAHHHHHHGAEEKLISEEDLNGA 267

RESULT 2

S41374
single chain Fv antibody - mouse
C:Species: Mus musculus (house mouse)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
C:Accession: S41374
R:Artsenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.
submitted to the EMBL Data Library, January 1994
A:Description: Construction and functional characterization of a single chain Fv antibody
A:Reference number: S41374

QY 63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYICAR----DYGA--YWGQGTIVTVSS 116
 DB 77 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYICARWGNPYPYAMDYWGQGTIVTVSS 136

RESULT 6
 B34871
 Ig heavy chain V region - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 15-Feb-1991 #sequence_revision 13-Sep-1991 #text_change 16-Aug-1996
 C:Accession: B34871
 R:Chaudhary, V.K.; Batra, J.K.; Gallo, M.G.; Willingham, M.C.; FitzGerald, D.J.; Pastan, Proc. Natl. Acad. Sci. U.S.A. 87, 1066-1070, 1990
 A:Title: A rapid method of cloning functional variable-region antibody genes in Escherichia coli
 A:Reference number: B34871; MUID:90138938; PMID:2105495
 A:Accession: B34871
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-121 <CHA>
 A:Cross-references: GB:M34000
 A:Note: the authors translated the codon GTG for residue 119 as Gly
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 32.2%; Score 522.5; DB 2; Length 121;
 Best Local Similarity 83.5%; Pred. No. 4.3e-28;
 Matches 101; Conservative 7; Mismatches 6; Indels 7; Gaps 2;

QY 3 EVKLQBSGGGLVQPGGRKUSCAASGFTFSFGHWVRQAPKGLWVAYISGSGSTIYY 62
 DB 1 DVQLVESGGGLVQPGGRKQLSCAASGFTFSFGHWVRQAPKGLWVAYISGSGNTIYY 60

QY 63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYICARD--YG-----AYWGQGTIVTVSS 115
 DB 61 ADTVKGRFTISRDNPKNTLFLQMTSLRSDDTMYICARSYYGYFYAMDYWGQGTIVTVSS 120

QY 116 S 116
 DB 121 S 121

RESULT 7
 JL0079
 Ig kappa chain precursor V region (anti-phenylloxazalone 6F6) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Dec-1991 #sequence_revision 09-Aug-1996 #text_change 16-Jul-1999
 C:Accession: JL0079; A43044; E49044
 R:Kaartinen, M.; Rocca-Serra, J.; Maekela, O. Mol. Immunol. 25, 859-865, 1988
 A:Title: Combinatorial association of V genes: one VH gene codes for three non-cross-reactive V genes
 A:Reference number: JL0076; MUID:89096973; PMID:3211160
 A:Accession: JL0079
 A:Molecule type: mRNA
 A:Residues: 1-130 <KAA>
 A:Cross-references: GB:M27792; NID:g197159
 A:Experimental source: mRNA clones for anti-phenylloxazalone antibody 6F6
 A:Note: the authors translated the codon TTC for residue 8 as Pro and TTC for residue 10 as Met
 A:Note: the codon given for 1-Met (AGT) is inconsistent with the authors' translation
 R:Malstein, C.; Even, J.; Jarvis, J.M.; Gonzalez-Fernandez, A.; Gherardi, E. Eur. J. Immunol. 22, 1627-1634, 1992
 A:Title: Non-random features of the repertoire expressed by the members of one V kappa gene
 A:Reference number: A49044; MUID:92289826; PMID:1601044
 A:Accession: A49044
 A:Molecule type: DNA
 A:Residues: 1-25 <MIL>
 A:Cross-references: GB:S37663; NID:g250214; PIDN:AAB22331.1; PID:g250217
 A:Note: sequence extracted from NCBI backbone (NCBIN:106802, NCBI:P:106809)
 A:Accession: B49044
 A:Molecule type: DNA
 A:Residues: 114-116 <MIL2>
 A:Cross-references: GB:S37664; NID:g250215; PIDN:AAB22332.1; PID:g250218
 A:Experimental source: BALB/c germ-line

A:Note: sequences extracted from NCBI backbone; partial nucleotide sequences of 13 add
 A:Note: sequence extracted from NCBI backbone (NCBIN:106807, NCBI:P:106822)
 C:Genetics:
 A:Gene: V(kappa)Ox1
 A:Introns: 17/1
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into 1 C:superfamily: immunoglobulin V region; immunoglobulin homology
 C:Superfamily: heterotetramer; immunoglobulin
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:123-130/Product: Ig kappa chain V region (6F6) #status predicted <MAT>
 F:138-111/Domain: immunoglobulin homology <IMM>
 F:45-109/Disulfide bonds: #status predicted

Query Match 31.8%; Score 516; DB 1; Length 130;
 Best Local Similarity 92.5%; Pred. No. 1.3e-27;
 Matches 99; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 133 IELTQSPAIMSASPGERVMTTCSSASSSVRYMNFQKSGTSPKRWIYDTSKLSSGVPARF 192
 DB 24 IVLTQSPAIMSASPGERVMTTCSSASSSVRYMNFQKSGTSPKRWIYDTSKLSSGVPARF 83

QY 193 SGGSGTSTSYSLTISSEAEADAATYYCQWSSNPLTFGAGTKLEKRA 239
 DB 84 SGGSGTSTSYSLTISSEAEADAATYYCQWSSNPLTFGAGTKLEKRA 130

RESULT 8
 S25058
 Ig kappa chain - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000
 C:Accession: S25058
 R:Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F. submitted to the EMBL Data Library, July 1992
 A:Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific
 A:Reference number: S25057
 A:Accession: S25058
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-235 <FIS>
 A:Cross-references: EMBL:X67211; NID:g54828; PIDN:CAA47650.1; PID:g54829
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F:38-111/Domain: immunoglobulin homology <IMM>

Query Match 31.7%; Score 514; DB 2; Length 235;
 Best Local Similarity 91.7%; Pred. No. 3.2e-27;
 Matches 100; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 133 IELTQSPAIMSASPGERVMTTCSSASSSVRYMNFQKSGTSPKRWIYDTSKLSSGVPARF 192
 DB 24 IVLTQSPAIMSASPGERVMTTCSSASSSVRYMNFQKSGTSPKRWIYDTSKLSSGVPARF 83

QY 193 SGGSGTSTSYSLTISSEAEADAATYYCQWSSNPLTFGAGTKLEKRAA 241
 DB 84 SGGSGTSTSYSLTISSEAEADAATYYCQWSSNPLTFGAGTKLEKRAA 132

RESULT 9
 A30562
 Ig kappa chain V regions (27.7.2 and 27.4b.2) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 21-Jan-2000
 C:Accession: A30562
 R:Siikder, S.K.; Borden, P.; Gruezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.J. J. Immunol. 142, 888-893, 1989
 A:Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen-b
 A:Reference number: A30562; MUID:89110066; PMID:2484031
 A:Accession: A30562
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-107 <SIK>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin
F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 31.5%; Score 511; DB 2; Length 107;
Best Local Similarity 91.5%; Pred. No. 2.2e-27;
Matches 97; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 133 IELTQSPAIMSASPGERVMTCTCSASSSVYNNWFQKSGTSPKRWIYDTSKLSSGVPARF 192
DB 2 IVLTQSPAIMSASPGERVMTCTCSASSSVYNNWFQKSGTSPKRWIYDTSKLSSGVPARF 61
QY 193 SSGSGGTSYSLTISSEAEADAATYCCQWSSNPLTFGAGTKLEK 238
DB 62 SSGSGGTSYSLTISSEAEADAATYCCQWSSNPLTFGAGTKLEK 107

RESULT 10

S29591
Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S29591

R;Kavaler, J.
submitted to the EMBL Data Library, April 1991

A;Reference number: S26459

A;Accession: S29591

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-103 <KAV>

A;Cross-references: EMBL:X59094; NID:952227; PID:CAA41820.1; PID:952228

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-88/Domain: immunoglobulin homology <IMM>

Query Match 31.3%; Score 508; DB 2; Length 103;
Best Local Similarity 94.2%; Pred. No. 3.3e-27;
Matches 97; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 133 IELTQSPAIMSASPGERVMTCTCSASSSVYNNWFQKSGTSPKRWIYDTSKLSSGVPARF 192
DB 1 IVLTQSPAIMSASPGERVMTCTCSASSSVYNNWFQKSGTSPKRWIYDTSKLSSGVPARF 60
QY 193 SSGSGGTSYSLTISSEAEADAATYCCQWSSNPLTFGAGTKLE 235
DB 61 SSGSGGTSYSLTISSEAEADAATYCCQWSSNPLTFGAGTKLE 103

RESULT 11

B49049

Ig kappa chain V region (anti-idiotypic) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000

C;Accession: B49049

R;Armandola, E.A.; Mariani, S.M.; Zwickl, M.; Hardman, N.; Ferrone, S.

Eur. J. Immunol. 22, 2893-2899, 1992

A;Title: Molecular analysis of anti-idiotypic monoclonal antibodies in the HLA-DR antigen

A;Reference number: A49049; MUID:93049629; PMID:1425914

A;Accession: B49049

A;Status: preliminary

A;Molecule type: nucleic acid

A;Residues: 1-104 <ARM>

A;Experimental source: BALB/c

C;Note: sequence extracted from NCBI backbone (NCBI:118298, NCBI:118299)

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: immunoglobulin

F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 31.3%; Score 508; DB 2; Length 104;
Best Local Similarity 94.2%; Pred. No. 3.4e-27;
Matches 97; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 133 IELTQSPAIMSASPGERVMTCTCSASSSVYNNWFQKSGTSPKRWIYDTSKLSSGVPARF 192
DB 1 IVLTQSPAIMSASPGERVMTCTCSASSSVYNNWFQKSGTSPKRWIYDTSKLSSGVPARF 60

DB 2 IVLTQSPAIMSASPGERVMTCTCSASSSVYNNWFQKSGTSPKRWIYDTSKLSSGVPARF 61
QY 193 SSGSGGTSYSLTISSEAEADAATYCCQWSSNPLTFGAGTKLE 235
DB 62 SSGSGGTSYSLTISSEAEADAATYCCQWSSNPLTFGAGTKLE 104

RESULT 12

PS0071

Ig kappa chain V region (38C13.V8) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000

C;Accession: PS0071

R;Levy, S.; Campbell, M.J.; Levy, R.

J. Exp. Med. 170, 1-13, 1989

A;Title: Functional immunoglobulin light chain genes are replaced by ongoing rearrangement

A;Reference number: A92781; MUID:89310348; PMID:2501443

A;Accession: PS0071

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-106 <LEV>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 31.2%; Score 506; DB 2; Length 106;
Best Local Similarity 92.4%; Pred. No. 4.7e-27;
Matches 97; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 133 IELTQSPAIMSASPGERVMTCTCSASSSVYNNWFQKSGTSPKRWIYDTSKLSSGVPARF 192
DB 2 IVLTQSPAIMSASPGERVMTCTCSASSSVYNNWFQKSGTSPKRWIYDTSKLSSGVPARF 61

QY 193 SSGSGGTSYSLTISSEAEADAATYCCQWSSNPLTFGAGTKLEK 237

DB 62 SSGSGGTSYSLTISSEAEADAATYCCQWSSNPLTFGAGTKLEK 106

RESULT 13

B30562

Ig kappa chain V region (27.10.2) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 21-Jan-2000

C;Accession: B30562

R;Sikder, S.K.; Borden, P.; Gruesz, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morris, S.

J. Immunol. 142, 888-893, 1989

A;Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen-b

A;Reference number: A30562; MUID:89110066; PMID:2464031

A;Accession: B30562

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-107 <SIK>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 31.2%; Score 506; DB 2; Length 107;
Best Local Similarity 89.6%; Pred. No. 4.7e-27;
Matches 95; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 133 IELTQSPAIMSASPGERVMTCTCSASSSVYNNWFQKSGTSPKRWIYDTSKLSSGVPARF 192
DB 2 IVLTQSPAIMSASPGERVMTCTCSASSSVYNNWFQKSGTSPKRWIYDTSKLSSGVPARF 61

QY 193 SSGSGGTSYSLTISSEAEADAATYCCQWSSNPLTFGAGTKLEK 238
DB 62 SSGSGGTSYSLTISSEAEADAATYCCQWSSNPLTFGAGTKLEK 107

RESULT 14

S11118

Ig kappa chain V region (clone NQ5-61.1.2) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C>Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 21-Jan-2000
C:Accession: S11118
R:Kaartinen, M.; Griffiths, G.M.; Markham, A.F.; Milstein, C.
Nature 304, 320-324, 1983
A:Title: mRNA sequences define an unusually restricted IgG response to 2-phenyloxazolone
A:Reference number: S07331; MUID:83271467; PMID:6877353
A:Accession: S11118
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-107 <KAA>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-89/Domain: immunoglobulin homology <IMM>

Query Match 30.9%; Score 501; DB 2; Length 107;
Best Local Similarity 91.5%; Pred. No. 1e-26;
Matches 97; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
Qy 133 IELTQSPAIMSASPGERVMTTCSSSVRYNMWFOCKSGTSPKRWIYDTSKLSSGVPARF 192
Db 2 IVLTSQPAIMSASPGKVTMTCSASSSVSYNMHWYCKSGTSPKRWIYDTSKLDSGVPARF 61
Qy 193 SGSGSGTSYSLTISSMFAEDAATYYCQWSSNPLTFGAGTKLELKR 238
Db 62 SGSGSGTSYSLTISSMFAEDAATYYCQWSSNPLTFGAGTKLELKR 107

RESULT 15

PC4405
Ig kappa chain V region (F3, anti-AFP) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 10-Nov-1997 #sequence_revision 23-Jan-1998 #text_change 21-Jan-2000
C:Accession: PC4405
R:Deng, J.B.; Han, H.; Su, C.Z.; Chen, C.Q.
Chinese Biochem. J. 12, 648-653, 1996
A:Title: Generation of a phage display library of the immunoglobulin repertoire from hum
A:Reference number: PC4405
A:Accession: PC4405
A:Molecule type: mRNA
A:Residues: 1-107 <DEN>
A:Experimental source: spleen cell
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-89/Domain: immunoglobulin homology <IMM>

Query Match 30.7%; Score 498; DB 2; Length 107;
Best Local Similarity 86.9%; Pred. No. 1.6e-26;
Matches 93; Conservative 7; Mismatches 7; Indels 0; Gaps 0;
Qy 132 DIELTQSPAIMSASPGERVMTTCSSSVRYNMWFOCKSGTSPKRWIYDTSKLSSGVPAR 191
Db 1 DIELTQSPAIMSASPGKVTMTCSASSSVSYNMHWYCKSGTSPKRWIYDTSKLDSGVPAR 60
Qy 192 FSGSGSGTSYSLTISSMFAEDAATYYCQWSSNPLTFGAGTKLELKR 238
Db 61 FSGSGSGTSYSLTISSMFAEDAATYYCQWSSNPLTFGAGTKLELKR 107

Search completed: May 27, 2004, 05:55:00
Job time : 35 secs

GenCore version 5.1.6
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OX protein - protein search, using sw model

Run on: May 27, 2004, 05:54:07 ; Search time 18 Seconds
(without alignments)
914.120 Million cell updates/sec

Title: US-09-403-882A-2
Perfect score: 1622
Sequence: 1 MAEVKLQESGGVLVQPGGSR.....VLTITSLILILMLQKKPR 316

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	535	33.0	136	1 HV16_MOUSE	P01783 mus musculus
2	507	31.3	107	1 KV6F_MOUSE	P04940 mus musculus
3	506	31.2	107	1 KV6H_MOUSE	P04942 mus musculus
4	502	30.9	107	1 KV6I_MOUSE	P04943 mus musculus
5	500	30.8	107	1 KV6G_MOUSE	P04941 mus musculus
6	494	30.5	107	1 KV6J_MOUSE	P04944 mus musculus
7	446	27.5	107	1 KV6C_MOUSE	P01677 mus musculus
8	441	27.2	107	1 KV6B_MOUSE	P01676 mus musculus
9	440	27.1	107	1 KV6D_MOUSE	P01678 mus musculus
10	436	26.9	107	1 KV6A_MOUSE	P01675 mus musculus
11	433	26.7	108	1 KV6K_MOUSE	P04945 mus musculus
12	428	26.4	107	1 KV6E_MOUSE	P01679 mus musculus
13	425	26.2	114	1 HV3B_HUMAN	P01763 homo sapien
14	423	26.1	122	1 HV3G_HUMAN	P01768 homo sapien
15	418	25.8	117	1 HV54_MOUSE	P18525 mus musculus
16	416	25.6	119	1 HV37_MOUSE	P01807 mus musculus
17	414.5	25.6	121	1 HV3J_HUMAN	P01771 homo sapien
18	412	25.4	117	1 HV55_MOUSE	P18526 mus musculus
19	410	25.3	126	1 HV3K_HUMAN	P01772 homo sapien
20	407.5	25.1	115	1 HV32_MOUSE	P01801 mus musculus
21	407	25.1	119	1 HV40_MOUSE	P01810 mus musculus
22	404.5	24.9	113	1 HV30_MOUSE	P01799 mus musculus
23	403	24.8	119	1 HV38_MOUSE	P01808 mus musculus
24	402.5	24.8	117	1 HV41_MOUSE	P01811 mus musculus
25	402	24.8	116	1 HV3T_HUMAN	P01781 homo sapien
26	401.5	24.8	97	1 HV56_MOUSE	P18527 mus musculus
27	400.5	24.7	113	1 HV27_MOUSE	P01796 mus musculus
28	400	24.7	129	1 KV4A_MOUSE	P01680 mus musculus
29	399.5	24.6	115	1 HV33_MOUSE	P01802 mus musculus
30	397.5	24.5	113	1 HV29_MOUSE	P01798 mus musculus
31	396.5	24.4	113	1 HV31_MOUSE	P01800 mus musculus
32	394.5	24.3	113	1 HV28_MOUSE	P01797 mus musculus
33	394.5	24.3	118	1 HV39_MOUSE	P01809 mus musculus

RESULT 1

HV16_MOUSE
 ID HV16_MOUSE STANDARD; PRT; 136 AA.
 AC P01783;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region MOPC 21 precursor (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81234548; PubMed=6788376;
 RA Botwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
 RA Baltimore D.;
 RT "Heavy chain variable region contribution to the NPB family of
 RT antibodies: somatic mutation evident in a gamma 2a variable region.";
 RL Cell 24:625-637(1981).
 RN [2]
 RP SEQUENCE OF 17-136.
 RX MEDLINE=77100368; PubMed=401950;
 RA Adetugbo K., Milstein C., Secher D.S.;
 RL "Molecular analysis of spontaneous somatic mutants.";
 RL Nature 265:299-304(1977).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; J00522; AAD15290.1; -
 DR PIR; E90809; GLMS21
 DR PDB; 1IGC; 03-JUN-95.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 DR Immunoglobulin V region; Signal; 3D-structure.
 KW NON_TER
 FT SIGNAL
 FT CHAIN
 FT DOMAIN
 FT DOMAIN
 FT DISULFID
 FT DISULFID
 FT CONFLICT
 FT CONFLICT
 FT CONFLICT
 FT NON_TER
 SQ SEQUENCE 136 AA; 15071 MW; 2276A98DBDBF7016 CRC64;
 IG HEAVY CHAIN V REGION MOPC 21.
 D SEGMENT.
 JH4 SEGMENT.
 HVAD -> DYAH (IN REF. 2).
 DN -> ND (IN REF. 2).
 W -> H (IN REF. 2).
 Y -> W (IN REF. 2).
 NON_TER 136
 SEQUENCE 136 AA; 15071 MW; 2276A98DBDBF7016 CRC64;


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CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted IGG response to 2-
RL Nature 304:320-324(1983).
CC -!- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
CC
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CC -----
CC EMBL; K00740; AAA38685.1; -.
DR HSSP; P01679; 2PBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 23
FT DOMAIN 24 33
FT DOMAIN 34 48
FT DOMAIN 49 55
FT DOMAIN 56 87
FT DOMAIN 88 96
FT DOMAIN 97 106
FT DISULFID 23 87
FT NON TER 107 107
SQ SEQUENCE 107 AA; 11572 MW; 6F694824ECFC08E6 CRC64;
Query Match 30.9%; Score 502; DB 1; Length 107;
Best Local Similarity 89.6%; Pred. No. 1.3e-30;
Matches 95; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
QY 133 IELTQSPAINASPGERVVTTCSSASSSVRYNNFQKSGTSPKRWIYDTSKLSSGVPARF 192
Db 2 IVLQSPAINASPGQKVVTTCSSASSSVYHMYQKSGTSPKRWIYDTSKLASGPARF 61
QY 193 SGSGSGTSYSLTISMEAEADAATYCCQWSSNPLTFGAGTKLELR 238
Db 62 SGSGSATSYSLTISMQAEDAATYCCQWSSNPLTFGAGTKLELR 107
RESULT 5
KV6G MOUSE STANDARD; PRT; 107 AA.
AC P04941;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 39, Last annotation update)
DE IG kappa chain V-VI region NQ2-48.2.2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted IGG response to 2-
RL Nature 304:320-324(1983).
CC -!- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
CC
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CC -----
CC EMBL; K00740; AAA38685.1; -.
DR HSSP; P01679; 2PBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 23
FT DOMAIN 24 33
FT DOMAIN 34 48
FT DOMAIN 49 55
FT DOMAIN 56 87
FT DOMAIN 88 96
FT DOMAIN 97 106
FT DISULFID 23 87
FT NON TER 107 107
SQ SEQUENCE 107 AA; 11572 MW; 6F694824ECFC08E6 CRC64;
Query Match 30.9%; Score 502; DB 1; Length 107;
Best Local Similarity 89.6%; Pred. No. 1.3e-30;
Matches 95; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
QY 133 IELTQSPAINASPGERVVTTCSSASSSVRYNNFQKSGTSPKRWIYDTSKLSSGVPARF 192
Db 2 IVLQSPAINASPGQKVVTTCSSASSSVYHMYQKSGTSPKRWIYDTSKLASGPARF 61
QY 193 SGSGSGTSYSLTISMEAEADAATYCCQWSSNPLTFGAGTKLELR 238
Db 62 SGSGSATSYSLTISMQAEDAATYCCQWSSNPLTFGAGTKLELR 107
RESULT 6
KV6J MOUSE STANDARD; PRT; 107 AA.
AC P04944;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-VI region NQ5-78.2.6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted IGG response to 2-
RL Nature 304:320-324(1983).
CC -!- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
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CC -----
CC EMBL; K00744; AAA38689.1; -.
DR HSSP; P01679; 2PBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
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CC -----
CC EMBL; K00737; AAA38682.1; -.
DR HSSP; P01679; 2PBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 23
FT DOMAIN 24 33
FT DOMAIN 34 48
FT DOMAIN 49 55
FT DOMAIN 56 87
FT DOMAIN 88 96
FT DOMAIN 97 106
FT DISULFID 23 87
FT NON TER 107 107
SQ SEQUENCE 107 AA; 11556 MW; 72488DA9EF354934 CRC64;
Query Match 30.8%; Score 500; DB 1; Length 107;
Best Local Similarity 89.6%; Pred. No. 1.8e-30;
Matches 95; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
QY 133 IELTQSPAINASPGERVVTTCSSASSSVRYNNFQKSGTSPKRWIYDTSKLSSGVPARF 192
Db 2 ILLTQSPAINASPGQKVVTTCSSASSSVYHMYQKSGTSPKRWIYDTSKLASGPARF 61
QY 193 SGSGSGTSYSLTISMEAEADAATYCCQWSSNPLTFGAGTKLELR 238
Db 62 SGSGSATSYSLTISMQAEDAATYCCQWSSNPLTFGAGTKLELR 107
RESULT 6
KV6J MOUSE STANDARD; PRT; 107 AA.
AC P04944;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-VI region NQ5-78.2.6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted IGG response to 2-
RL Nature 304:320-324(1983).
CC -!- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; K00744; AAA38689.1; -.
DR HSSP; P01679; 2PBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
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DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG LIKE; 1.
 KW Immunoglobulin V region; Hybridoma.
 FT DOMAIN 1 23
 FT DOMAIN 24 33
 FT DOMAIN 34 48
 FT DOMAIN 49 55
 FT DOMAIN 56 87
 FT DOMAIN 88 96
 FT DOMAIN 97 106
 FT DISULFID 23 87
 FT NON TER 107 107
 SQ SEQUENCE 107 AA; A38290781F3C30D3 CRC64;

Query Match 30.5%; Score 494; DB 1; Length 107;
 Best Local Similarity 87.7%; Pred. No. 4.9e-30;
 Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 133 IELTQSPAIMSASPCGERTVMTCSASSSVRYNWNFQKSGTSPKRWIYDTSKLSSGVPARF 192
 Db 2 ILLTQSPAIMSASPCQKVTMTCSASSSVYHWHYQKSGTSPKRWIYDTSKLSSGVPARF 61

QY 193 SCGSGGTSYSLTSSMEAEADATYYCQWSSNPLTFGAGTKLELKR 238
 Db 62 XGSGATSYSLTSSMEAEADATYYCQWSSNPLTFGSGTKLEKR 107

RESULT 7
 KV6C_MOUSE
 ID KV6C_MOUSE STANDARD; PRT; 107 AA.
 AC P01677;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-VI region TEPC 601/TEPC 191.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE (TEPC 601).
 RX MEDLINE=79082830; PubMed=103573;
 RA Rao D.N., Rudikoff S., Potter M.;
 RT "k Chain variable regions from three galactan binding myeloma
 proteins.";
 RL Biochemistry 17:5555-5559(1978).
 RN [2]
 RP SEQUENCE (TEPC 191).
 RX MEDLINE=81054757; PubMed=6776525;
 RA Rudikoff S., Rao D.N., Glaudemans C.P.J., Potter M.;
 RT "kappa Chain joining segments and structural diversity of antibody
 combining sites.";
 RL Proc. Natl. Acad. Sci. U.S.A. 77:4270-4274(1980).
 CC - MISCELLANEOUS; THE TWO SEQUENCES ARE IDENTICAL.
 CC - MISCELLANEOUS; THESE CHAINS WERE ISOLATED FROM MYELOMA PROTEINS
 CC THAT BIND GALACTAN.

DR HSP; P01679; 2FBJ.
 DR INTERPRO; IPR007110; IG-like.
 DR INTERPRO; IPR003596; IG_V.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 33
 FT DOMAIN 34 48
 FT DOMAIN 49 55
 FT DOMAIN 56 87
 FT DOMAIN 88 96
 FT DOMAIN 97 106
 FT DISULFID 23 87
 FT NON TER 107 107
 SQ SEQUENCE 107 AA; 11568 MW; 203CD752A5EC34D7 CRC64;

Query Match 27.5%; Score 446; DB 1; Length 107;
 Best Local Similarity 80.4%; Pred. No. 1.7e-26;
 Matches 86; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 132 DIELTQSPAIMSASPCGERTVMTCSASSSVRYNWNFQKSGTSPKRWIYDTSKLSSGVPAR 191
 Db 1 EIVLTQSPAITAASLGQKVTITCSASSSVYHWHYQKSGTSPKRWIYDTSKLSSGVPAR 60

QY 192 FSGSGGTSYSLTSSMEAEADATYYCQWSSNPLTFGAGTKLELKR 238
 Db 61 FSGSGGTSYSLTSSMEAEADATYYCQWSSNPLTFGAGTKLELKR 107

RESULT 8
 KV6B_MOUSE
 ID KV6B_MOUSE STANDARD; PRT; 107 AA.
 AC P01676;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-VI region XRPC 24.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=79082830; PubMed=103573;
 RA Rao D.N., Rudikoff S., Potter M.;
 RT "k Chain variable regions from three galactan binding myeloma
 proteins.";
 RL Biochemistry 17:5555-5559(1978).
 CC - MISCELLANEOUS; THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
 CC BIND GALACTAN.

DR HSP; P01679; 2FBJ.
 DR INTERPRO; IPR007110; IG-like.
 DR INTERPRO; IPR003596; IG_V.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 33
 FT DOMAIN 34 48
 FT DOMAIN 49 55
 FT DOMAIN 56 87
 FT DOMAIN 88 96
 FT DOMAIN 97 106
 FT DISULFID 23 87
 FT NON TER 107 107
 SQ SEQUENCE 107 AA; 11584 MW; 36B6D022A5EC34D7 CRC64;

Query Match 27.2%; Score 441; DB 1; Length 107;
 Best Local Similarity 78.5%; Pred. No. 4.1e-26;
 Matches 84; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

QY 132 DIELTQSPAIMSASPCGERTVMTCSASSSVRYNWNFQKSGTSPKRWIYDTSKLSSGVPAR 191
 Db 1 EIVLTQSPAITAASLGQKVTITCSASSSVYHWHYQKSGTSPKRWIYDTSKLSSGVPAR 60

QY 192 FSGSGGTSYSLTSSMEAEADATYYCQWSSNPLTFGAGTKLELKR 238
 Db 61 FSGSGGTSYSLTSSMEAEADATYYCQWSSNPLTFGAGTKLELKR 107

RESULT 9
 KV6D_MOUSE
 ID KV6D_MOUSE STANDARD; PRT; 107 AA.
 AC P01678;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)

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DE Ig kappa chain V-VI region SAPC 10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=8105457; PubMed=6776525;
RA Rudikoff S., Rao D.N., Glaudemans C.P.J., Potter M.;
RT "Kappa Chain joining segments and structural diversity of antibody
RT combining sites";
RL Proc. Natl. Acad. Sci. U.S.A. 77:4270-4274 (1980).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BIND GALACTAN.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 24 33
FT COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 34 48
FT COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 56 87
FT COMPLEMENTARITY-DETERMINING-4.
FT DISULFID 23 87
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11554 MW; 27A2D022A5EC34D7 CRC64;

Query Match 27.1%; Score 440; DB 1; Length 107;
Best Local Similarity 78.5%; Pred. No. 4.8e-26;
Matches 84; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

QY 132 DIETQSPALMSASGERVMTCSASSSVRYMNFQKSGTSPKRWIYDTSKLSSGVPAR 191
DB 1 EIVTQSPALTAASLGQKVTITCSASSSVYMHYQKSGTSPKRWIYEIKLASGVPAR 60

QY 192 FSGSGGTSYSLTSSMEADAATYYCQWSSNPLTFGAGTKLEIKR 238
DB 61 FSGSGGTSYSLTSSMEADAATYYCQWNYPLTFGGTKLEIKR 107

RESULT 10
KV6A MOUSE STANDARD; PRT; 107 AA.
AC P01675;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region XRPC 44.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79082830; PubMed=103573;
RA Rao D.N., Rudikoff S., Potter M.;
RT "k Chain variable regions from three galactan binding myeloma
RT proteins";
RL Biochemistry 17:5555-5559 (1978).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BIND GALACTAN.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
DR PROSITE; PS50835; IG_LIKE; 1.

QY 132 DIETQSPALMSASGERVMTCSASSSVRYMNFQKSGTSPKRWIYDTSKLSSGVPAR 191
DB 1 EIVTQSPALTAASLGQKVTITCSASSSVYMHYQKSGTSPKRWIYEIKLASGVPAR 60

QY 192 FSGSGGTSYSLTSSMEADAATYYCQWSSNPLTFGAGTKLEIKR 238
DB 61 FSGSGGTSYSLTSSMEADAATYYCQWNYPLTFGGTKLEIKR 107

RESULT 10
KV6A MOUSE STANDARD; PRT; 107 AA.
AC P01675;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region XRPC 44.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=8105457; PubMed=6776525;
RA Rudikoff S., Rao D.N., Glaudemans C.P.J., Potter M.;
RT "Kappa Chain joining segments and structural diversity of antibody
RT combining sites";
RL Proc. Natl. Acad. Sci. U.S.A. 77:4270-4274 (1980).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BIND GALACTAN.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
DR PROSITE; PS50835; IG_LIKE; 1.

QY 132 DIETQSPALMSASGERVMTCSASSSVRYMNFQKSGTSPKRWIYDTSKLSSGVPAR 191
DB 1 EIVTQSPALTAASLGQKVTITCSASSSVYMHYQKSGTSPKRWIYEIKLASGVPAR 60

QY 192 FSGSGGTSYSLTSSMEADAATYYCQWSSNPLTFGAGTKLEIKR 238
DB 61 FSGSGGTSYSLTSSMEADAATYYCQWNYPLTFGGTKLEIKR 107

RESULT 11
KV6K MOUSE STANDARD; PRT; 108 AA.
AC P04945;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region NQ2-6.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted Igg response to 2-
RT phenylloxazone and its early diversification.";
RL Nature 304:320-324 (1983).
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CC -----
CC EMBL; K00746; AAA38691.1; -.
CC HSSP; P01679; 2FBJ.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; Ig; 1.
CC PROSITE; PS50835; IG_LIKE; 1.
CC Immunoglobulin V region; Hyridoma.
KW DOMAIN 1 23
KW COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 24 33
FT COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 49 55
FT COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 56 87
FT COMPLEMENTARITY-DETERMINING-4.
FT DISULFID 23 87
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11713 MW; DABF235CD9680AC6 CRC64;

Query Match 26.7%; Score 433; DB 1; Length 108;

```

```
Best Local Similarity 80.4%; Pred. No. 1.6e-25;
Matches 86; Conservative 8; Mismatches 11; Indels 2; Gaps 1;

QY 133 IELTQSPAIMGASPERVTMTCSASSVRYNNWFQKSGTSPKRWIYDTSKLSSGVPAF 192
DB 2 ILLTQSPAIMGASPGQKVTITCSASSSVYNNWFQKSGTSPKRWIYDTSKLSSGVPAF 61

QY 193 SGSGSGTSYSLTISMEADATYCCQWSSNP--LTFGAGTKLELK 237
DB 62 SGSGSGTSYSLTITKQAEADATYCCQWSSNP--LTFGAGTKLELK 108

RESULT 12
KV6E MOUSE STANDARD; PRT; 107 AA.
AC P01679;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE IG kappa chain V-VI region J539.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=81054757; PubMed=6776525;
RA Rudikoff S., Rao D.N., Glaudemans C.P.J., Potter M.;
RT "Kappa Chain joining segments and structural diversity of antibody
PT combining sites.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:4270-4274 (1980).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RX MEDLINE=88217852; PubMed=3449853;
RA Suh S.W., Bhat T.N., Navia M.A., Cohen G.H., Rao D.N., Rudikoff S.,
RA Davies D.R.;
RT "The galactan-binding immunoglobulin Fab J539: an X-ray diffraction
PT study at 2.6-A resolution.";
RL Proteins 1:74-80 (1986).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BIND GALACTAN.
DR PIR; A01942; KWSJ5.
DR PDB; 2PEJ; 15-OCT-90.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; 3D-structure.
FT DOMAIN 1 23
FT DOMAIN 24 33
FT DOMAIN 34 48
FT DOMAIN 49 55
FT DOMAIN 56 87
FT DOMAIN 88 96
FT DOMAIN 97 106
FT DISULFID 23 87
FT STRAND 4 7
FT STRAND 10 14
FT TURN 15 16
FT STRAND 19 25
FT STRAND 31 37
FT TURN 39 40
FT STRAND 44 48
FT TURN 49 51
FT STRAND 52 53
FT TURN 55 56
FT STRAND 59 60
FT STRAND 61 66
FT TURN 67 68
FT STRAND 69 74
FT TURN 79 81
FT HELIX 81 91
FT STRAND 83 91

Query Match 26.4%; Score 428; DB 1; Length 107;
Best Local Similarity 76.6%; Pred. No. 3.7e-25;
Matches 82; Conservative 14; Mismatches 11; Indels 0; Gaps 0;

QY 132 DIELTQSPAIMGASPERVTMTCSASSVRYNNWFQKSGTSPKRWIYDTSKLSSGVPAF 191
DB 1 EIVLTQSPAITAASLGQKVTITCSASSSVSLHWYQKSGTSPKRWIYDTSKLSSGVPAF 60

QY 192 FSGSGSGTSYSLTISMEADATYCCQWSSNP--LTFGAGTKLELK 238
DB 61 FSGSGSGTSYSLTITMEADATYCCQWSSNP--LTFGAGTKLELK 107

RESULT 13
HV3B HUMAN STANDARD; PRT; 114 AA.
AC F01783;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V-III region WEA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=83273707; PubMed=6410398;
RA Goni F., Francione B.;
RT "Amino acid sequence of the Fv region of a human monoclonal IgM
PT (protein WEA) with antibody activity against 3,4-pyruvylated
RL galactose in Klebsiella polysaccharides K30 and K33.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841 (1983).
CC -!- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
CC AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
CC WALDENSTROM'S MACROGLOBULINEMIA.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02046; M3HUWE.
DR HSSP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT DOMAIN 1 112
FT MOD RES 1 112 PYRROLIDONE CARBOXYLIC ACID.
FT NON-TER 114 114
FT SEQUENCE 114 AA; 12256 MW; D88294FB418A07B7 CRC64;

Query Match 26.2%; Score 425; DB 1; Length 114;
Best Local Similarity 68.4%; Pred. No. 6.7e-25;
Matches 78; Conservative 20; Mismatches 16; Indels 0; Gaps 0;

QY 3 EVKLQSSGGGLVQPGSKRLSCAASGFTFSFGHHWVROAPEKGLWYAYISSGSIY 62
DB 1 QVLVDSSGGGLVEPGSKRLSCAASGFTFSFGHHWVROAPEKGLWYAYISSGSIY 60

QY 63 ADTVKGRFTISRDNPKNTLFQMTSLRSEDVYMYCARDYGYWGQGTIVTVSS 116
DB 61 ADSVKGRFTISRDNBSKNSLYLQMSLRADTAIVYCARGLLWQGLIVTVSS 114

RESULT 14
```

QY	3	EYKLESGGLVQPGGSRKLSCAASGTTFSFGHWWYRQAPKGLBWWAYISGSGSTIYV	62
DB	1	QVELVESGGVYVFGRSRLSLSCAASGTTFSFNAMHWYRPPGKGLBWWAVISYBGBBKYY	60
QY	63	ADTVKGRITISRDNPNTLFLQMTSLRSLEDVWYVCARD---	114
DB	61	ABSVKGRITISDSSKTYLQMSLRASSTAVYVCARDRLYGBYRNFYWGQGLTVTV	120
QY	115	SS 116	
DB	121	SS 122	

RESULT	15				
HV54	MOUSE	STANDARD;	PRT;	117	AA.
ID	HV54	MOUSE			
AC	P18525;				
DT	01-NOV-1990	(Rel. 16, Created)			
DT	01-NOV-1990	(Rel. 16, Last sequence update)			
DT	15-JUL-1999	(Rel. 38, Last annotation update)			
DE	19 heavy chain V region 5-84 precursor.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
NCBI	TXID=10090;				
RN	[1] _				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=BA16/cj;				
RX	MEDLINE=89279149; PubMed=2499654;				
RA	Levy N.S., Mailpero U.V., Lebecque S.G., Gearhart P.J.;				
RT	"Early onset of somatic mutation in immunoglobulin VH genes during				
RT	the primary immune response."				

```

J. Exp. Med. 169:2007-2019(1989)).
CC -I- MISCELLANEOUS; THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIN; JTO505; HVMS84.
DR HSP; P01810; 2PEJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SMC0406; IGv; 1.
DR PROSITE; PS50835; IG_Like; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 5-84.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12872 MW; 234055CB6A469861 CRC64;

Query Match 25.8%; Score 418; DB 1; Length 117;
Best Local Similarity 79.0%; Pred. No. 2.3e-24;
Matches 79; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

QY 1 MAEVKLQESGGGLVQPGGSRKLSCAASGFTFSFGHHWTRQAEPKGLEWVAI$SSGSSTI 60
   : |||||
Db 18 LCEVKLVESGGGLVQPGGSLKLSCAASGFTFSYSYTWMSVRQTPEKRLEWVAI$SNGGGST 77
   : |||||
QY 61 YYADTVKGRITISRDNPNTLFLQMTSLRSEDVTWYYCAR 100
   : |||||
Db 78 YYPDTVKGRITISRDNAKNLYIQMSSLKSEDTAMYYCAR 117
   : |||||

Search completed: May 27, 2004, 05:57:06
Job time : 20 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 27, 2004, 05:54:07 ; Search time 50 Seconds
(without alignments)
1994.075 Million cell updates/sec

Title: US-09-403-882A-2
Perfect score: 1622
Sequence: 1 MAEVKLESGGLVQPGGSR.....VLTITSLILMLMOKKPR 316

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

- 1: sp_archea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	853.5	52.6	298	11 Q9QYF0	Q9QYF0 mus musculus
2	695	42.8	241	11 Q921A6	Q921A6 mus musculus
3	658	40.6	243	11 Q7TQM2	Q7TQM2 mus musculus
4	608.5	37.5	218	11 Q925S1	Q925S1 mus musculus
5	542	33.4	473	11 Q91Z05	Q91Z05 mus musculus
6	498	30.7	112	11 Q8K1F0	Q8K1F0 mus musculus
7	491	30.3	235	11 Q91W12	Q91W12 mus musculus
8	484.5	29.9	487	11 Q93KA4	Q93KA4 mus musculus
9	483	29.8	134	11 Q8VDD0	Q8VDD0 mus musculus
10	480	29.6	112	11 Q8K1F2	Q8K1F2 mus musculus
11	462.5	28.5	113	4 Q9UL90	Q9UL90 homo sapien
12	462	28.5	613	4 Q8WUK1	Q8WUK1 homo sapien
13	461	28.4	112	11 Q8K1F3	Q8K1F3 mus musculus
14	458	28.2	114	11 Q8K1F1	Q8K1F1 mus musculus
15	454.5	28.0	437	11 Q9P1A4	Q9P1A4 mus musculus
16	454.5	28.0	597	4 Q96BB9	Q96BB9 homo sapien

17	452.5	27.9	119	11 Q920E7	Q920E7 mus musculus
18	445	27.4	118	4 Q9UL91	Q9UL91 homo sapien
19	443	27.3	479	11 Q91WP5	Q91WP5 mus musculus
20	440.5	27.2	116	4 Q9UL93	Q9UL93 homo sapien
21	439.5	27.1	494	4 Q96K68	Q96K68 homo sapien
22	439	27.1	486	11 Q91207	Q91207 mus musculus
23	438.5	27.0	131	11 Q811C3	Q811C3 mus musculus
24	437	26.9	106	5 Q9U410	Q9U410 schistosoma
25	433.5	26.7	147	4 Q9V509	Q9V509 homo sapien
26	429	26.4	487	11 Q80Z17	Q80Z17 mus musculus
27	428	26.4	235	11 Q7TMK0	Q7TMK0 mus musculus
28	428	26.4	573	4 Q8WU38	Q8WU38 homo sapien
29	424	26.1	480	11 Q91XE1	Q91XE1 mus musculus
30	422	26.0	122	4 Q9UL84	Q9UL84 homo sapien
31	421.5	26.0	121	4 Q9UL71	Q9UL71 homo sapien
32	416	25.6	499	4 Q8N5K4	Q8N5K4 homo sapien
33	415	25.6	118	4 Q9UL72	Q9UL72 homo sapien
34	410	25.3	493	4 Q8NCL6	Q8NCL6 homo sapien
35	405	25.0	470	4 Q7Z5W1	Q7Z5W1 homo sapien
36	401.5	24.8	97	11 Q9JL76	Q9JL76 mus musculus
37	398.5	24.6	469	11 Q8R3V9	Q8R3V9 mus musculus
38	395	24.4	112	4 Q9HCC1	Q9HCC1 homo sapien
39	393.5	24.3	479	11 Q7TMK4	Q7TMK4 mus musculus
40	390.5	24.1	484	11 Q6VEA0	Q6VEA0 mus musculus
41	385	23.7	482	4 Q7Z351	Q7Z351 homo sapien
42	378.5	23.3	170	11 Q925S2	Q925S2 mus musculus
43	376	23.2	95	4 Q9ULB6	Q9ULB6 homo sapien
44	375.5	23.2	521	4 Q8N4Y9	Q8N4Y9 homo sapien
45	367.5	22.7	131	4 Q9UL88	Q9UL88 homo sapien

ALIGNMENTS

RESULT 1

Q9QYF0 PRELIMINARY; PRT; 298 AA.

ID Q9QYF0; AC Q9QYF0; DT 01-MAY-2000 (TRENBLrel. 13, Created)

DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)

DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)

DE CN 8 scFv.

OS CN 8.

OS Mus musculus (Mouse)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Balb/c; TISSUE=Spleen;

EX MEDLINE=20183931; PubMed=10706631;

RA Shinohara N., Demura T., Fukuda H;

RT "Isolation of a vascular cell wall-specific monoclonal antibody

RT recognizing a cell polarity by using a phage display subtraction

RT method."

RL Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).

DR EMBL; AB036341; BAA86633.1; --

DR PIR; A33933; A33933.

DR PIR; S19112; S19112.

DR HSRF; P01607; IREI.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; Ig; 2.

DR SMART; SM00406; IGV; 2.

DR PROSITE; PS00635; IG LIKE; 2.

SQ SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;

Query Match 52.6%; Score 853.5; DB 11; Length 298;

Best Local Similarity 66.3%; Pred. No. 8.9e-60;

Matches 163; Conservative 32; Mismatches 46; Indels 5; Gaps 2;

Qy 1 MAEVKLESGGLVQPGGSRKLSAASGFTFSFGMHWVTCQAEKGLWVAYVSSGSSI 60

D	b	38	MAQVKLQQSGGGLVTPGGSLKSCAASGSDFSRVMWSVRQAPGKGLWEGINPDSSIT	97	
Q	y	61	YYADTVKGRFTTISRDNPKNTLFLQMTSLRSSEDTVMYICAR----	DYGAYWGQGTITVTSSS	116
D	b	98	NYPSPSKDKFIISRDNAKNLTLYQMSKYRSEDATLYICARASYGHSA	YWGGTTVTSSS	157
Q	y	117	GGGSGGGSGGGSDIELTQSPALMSASPERRVTMCSSASSSV-RYMNWFQOKSGTSPK	175	
D	b	158	GGGSGGGSGGGSDIELTQSPALSASVGETVTITCRASGNHNLAWYQOKQKSPQ	217	
Q	y	176	RWIYDTSKLSSGVPAFPFGSGSGSYSLTISSMEAEADAATVCYOQSSNPLTFGAGTKLE	235	
D	b	218	LLVYNAKTLADGPFRFSGSGGTQYSKLNSLOPEDFGSYCHQFWTIPYTFGGGKTLE	277	
Q	y	236	LXRAAA	241	
D	b	278	IKRAAA	283	
RESULT 2					
O	921A6	PRELIMINARY; PRT; 241 AA.			
I	D	Q921A6;	AC		
D	T	01-DEC-2001 (TREMBLrel. 19, Created)			
D	T	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
D	T	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
D	E	Anti-CEA 79 single chain Fv fragment (Fragment).			
O	S	Mus musculus (Mouse).			
O	C	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
O	C	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
O	X	NCBI_TaxId:10090;			
R	N	[1]			
R	P	SEQUENCE FROM N.A.			
R	X	MEDLINE=98170165; PubMed=9509426;			
R	A	Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,			
R	A	Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;			
R	T	"Cloning and characterization of cDNAs encoding VH and VL of a			
R	T	monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and			
R	L	generation of a single-chain Fv molecule (scFv).";			
R	L	Mol. Cells 7:816-819(1997).			
D	R	EMBL; U88067; AAB48044.1; -			
D	R	InterPro; IPR007110; IG-like.			
D	R	InterPro; IPR003596; IG_v.			
D	R	Pfam; PF00047; IG_2.			
D	R	SMART; SM00406; IGV; 2.			
D	R	PROSITE; PS50835; IG_LIKE; 2.			
F	T	NON_TER	1		
F	T	NON_TER	241		
S	Q	SEQUENCE	241 AA; 26086 MW; 0276887248ESC771 CRC64;		
Query Match					
Best Local Similarity 42.8%; Score 695; DB 11; Length 241;					
Matches 137; Conservative 40; Mismatches 55; Indels 14; Gaps					
Q	y	3	EVLKIQESGGGLVQPGSKLKSCAASGPTFFSFGMHVYRQAPEKGLEVAIVISSGSTIYY	62	
D	b	1	QVKLGQGBELKPKGETVKISKASGYFTTDYGMNVKQAPGKGLKWGWINTYTGEPTY	60	
Q	y	63	ADTVKGRFTTISRDNPKNTLFLQMTSLRSSEDTVMYICARD----	YGAYWGQGTITVTSSGG	118
D	b	61	ADDFKGRFAFSLETSSATYLQINNLNKNEIDATFYCARKKOLLRYFDYWGQGTITVTSSGG	120	
Q	y	119	GSGGGGGSGGGSDIELTQSPALMSASPERRVTTCSSASSV-RYMNWFQOKSGTSPKR-	176	
D	b	121	GSGGGGGSGGGSDIELTQSPSSLASIGGKVTTCKASQDINKITYAWYQHKGKGFPSA	180	
Q	y	177	---WIYDTSKLSSGVPAFPFGSGSGTYSYSLTISSMEAEADAATVCYOQSSNPLTFGAGTK	233	
D	b	181	HTHIY-----IQGPIPSFGSGSGRDIYSPGISNLEPEDIATYCLEY-DNLHTFGGKT	235	
Q	y	234	LEKRA	239	
D	b	236	LEKRA	241	

RT of the irradiated mice by treatment with the intestinal RNA of mice of the same strain."

RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80 (2001).

DR EMBL; AF240168; AA43733.1; .

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; Ig; 2.

DR SMART; SMO0406; IGV; 1.

DR PROSITE; PS00835; IG LIKE; 1.

FT NON TER 218

SQ SEQUENCE 218 AA; 527E4FABF7982817 CRC64;

Query Match 37.5%; Score 608.5; DB 11; Length 218;

Best Local Similarity 55.5%; Pred. No. 1.8e-40;

Matches 121; Conservative 33; Mismatches 55; Indels 9; Gaps 3;

QY 1 MAEVKQESGGGLVQPGSGKLSCAASGPTFFSFGHWHVRQAPEKGLWVAISSGSSTI 60

DB 1 YAQVKQSGPELKKGGETVRISCKASGYFTTAGQWQVQKPGKLGKWINTHSGVP 60

QY 61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYICAR-DYG---AYWGGGTTVTSS 116

DB 61 KYAEFPKGRPAFLSASTAYLQISNLKNEATATVFCMRWDYDGGFAVWGGGTTVTSS 120

QY 117 GGGSGGGGGGGGGDIETQSPAIMSASGERVTWTCSSASSV-----RYNWFQOKSG 171

DB 121 GGGSGGGGGGGGGDIETQSPAIMSASGERVTWTCSSASSV-----RYNWFQOKSG 171

QY 172 TSPKRWIYDTSKLSGGVPARFSGSGTSYSLTISSE 209

DB 181 QPKLLIYAASKQSGVPAGLLASGSGTDFSLNIYPME 218

RESULT 5

Q91Z05 PRELIMINARY; PRT; 473 AA.

AC Q91Z05; 01-DEC-2001 (Tremblrel. 19, Created)

DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)

DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)

DE Hypothetical protein.

GN AU044919.

OS Mus musculus (Mouse).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Strausberg R.; Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

RL EMBL; BC010327; AAH10327.1; .

DR MGD; MGI; 2144967; AU044919.

DR GO; GO:0005489; P:electron transporter activity; IEA.

DR GO; GO:0006118; P:electron transport; IEA.

DR InterPro; IPR000345; Cyt c heme_B.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; Ig; 3.

DR SMART; SMO0406; IGV; 1.

DR PROSITE; PS00190; CYTOCHROME C; 1.

DR PROSITE; PS00835; IG LIKE; 4.

DR PROSITE; PS00290; IG_MHC; 1.

KW Hypothetical protein_

SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match 33.4%; Score 542; DB 11; Length 473;

Best Local Similarity 51.7%; Pred. No. 9.3e-35;

Matches 120; Conservative 20; Mismatches 52; Indels 40; Gaps 5;

QY 3 EVKLQESGGGLVQPGSGKLSCAASGPTFFSFGHWHVRQAPEKGLWVAISSGSSTIY 62

DB 20 EVLVESGGGLVQPGSGKLSCAASGPTFFSDYGMHWHVRQAPEKGLWVAISSGSSTIY 79

QY 63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYICARDYCA-----YWGQGTIVTSSGG 118

DB 80 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYICARELWLRIDYWGQGTIVTSSA- 138

QY 119 GSGGGGGGGGGDIETQSPAIMSASGERVTWTCSSASSSVRYNWFQOKSGTSPKRWI 178

DB 139 -----KTPPSVYPLAPGCGDTGTGSSVTGLCGLVKGYFPESVTI----- 177

QY 179 YDTSKLSGGV---PARFSGSGGTSYSLTISSEMEADAATYYCQWSSNPLT 227

DB 178 WNSGLSSSVHTFPALQSLYTWSSSVTPES-----STWPSQTVT 218

RESULT 6

Q8K1F0 PRELIMINARY; PRT; 112 AA.

AC Q8K1F0; 01-OCT-2002 (Tremblrel. 22, Created)

DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)

DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)

DE Anti-Vipase light chain variable region (Fragment).

OS Mus musculus (Mouse).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BALB/c; TISSUE=Hyperimmunized spleen;

RA Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.; "Inmate proteolytic antibodies: Failed D-vipase response to the D-entantionmer of VIP and identification of L-vipase VL domains."

RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF516285; AAM64203.1; .

DR PIR; A33933; A33933.

DR InterPro; IPR003599; Ig-like.

DR InterPro; IPR007110; Ig_v.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; Ig; 1.

DR SMART; SMO0409; IGV; 1.

DR SMART; SMO0406; IGV; 1.

DR PROSITE; PS00835; IG LIKE; 1.

FT NON TER 1

FT NON TER 112

SQ SEQUENCE 112 AA; 11901 MW; F6644663201AA239 CRC64;

Query Match 30.7%; Score 498; DB 11; Length 112;

Best Local Similarity 88.8%; Pred. No. 4.5e-32;

Matches 95; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 135 LTQSPAIMSASGERVTWTCSSASSSVRYNWFQOKSGTSPKRWIYDTSKLSGGVPARFSG 194

DB 4 LTQSPAIMSASGERVTWTCSSASSSVRYNWFQOKSGTSPKRWIYDTSKLSGGVPARFSG 63

QY 195 SSGTSYSLTISSEMEADAATYYCQWSSNPLTFGAGTKLELRAAA 241

DB 64 SSGTSYSLTISSEMEADAATYYCQWSSNPLTFGAGTKLELRAAA 110

RESULT 7

Q91W12 PRELIMINARY; PRT; 235 AA.

AC Q91W12; 01-DEC-2001 (Tremblrel. 19, Created)

DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)

DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)

DE Hypothetical protein.

OS Mus musculus (Mouse).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

```
RC TISSUE=Breast tumor;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006643; AAH06643.1; -.
DR PDB; 1AY1; 30-JAN-02.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS0835; IG LIKE; 2.
DR PROSITE; PS0290; IG_MHC; 1.
KW Hypothetical protein.
SQ
  Query Match      30.3%; Score 491; DB 11; Length 235;
  Best Local Similarity 87.2%; Pred. No. 4.2e-31;
  Matches 95; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 133 IELTOSPAIMASPGERTVMTCSASSSVRYNWNFQKSGTSPKRWIYDTKLSGVPARF 192
DB 24 IVLTSPIAMSGPGRVTMTCSASSSVSHMHYQKSGTSPKRWIYDTFKLTSGVDRF 83

QY 193 SGSGSGTGYSLTISMEAEADATYCCQWSSNPLTFGAGTKLELKRAAA 241
DB 84 SGSGSGTGYSLTISNWEAEADATYCCQWSSNPLTFGAGTKLELKRAA 132

RESULT 8
Q99KA4 PRELIMINARY; PRT; 487 AA.
AC Q99KA4;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP STRAIN=BALB/c;
RA Chernajovsky Y.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [12]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Sembi P.;
RT "Targeting T cells to the CNS.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ416331; CAC94866.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS0835; IG LIKE; 1.
DR PROSITE; PS0290; IG_MHC; 2.
KW Hypothetical protein.
SQ
  Query Match      29.9%; Score 484.5; DB 11; Length 487;
  Best Local Similarity 41.6%; Pred. No. 3.6e-30;
  Matches 124; Conservative 23; Mismatches 72; Indels 79; Gaps 11;

QY 3 EVKLQESGGVLVQGGKLSKASGTFSSFGNHWVRQAPKGLWAVISSGSTIYY 62
DB 20 EVQLVESGGGLVQPGGSLKLSKASGTFSSYAMSVRQTPKRLWVATISDGGSTYY 79

QY 63 ADTVKGRFTISRDNPKNFTPLQMTSLRSDEDTVMYICARDYGA-----YWGQGTIV 112
DB 80 PDNVKGRFTISRDNAKKNLYIQMHLKASEDTAMVICARDMGSPYGGYSRFDYWGQTTI 139

QY 113 TVSSGGGGGGGGGGGGSDIELTQSPAI-----MSASPGERTVMTCSASSSVRYN 164
DB 140 TVSS-----ESARNPTIPLTLPRALSDP---VIIGLIH-----D 173

QY 165 WFQKSGTSPKRWIYDTKLSGSGV-----PARPSGSGSGTGYSLTISMEAEADATYIC 218

Query Match      29.8%; Score 483; DB 11; Length 134;
Best Local Similarity 86.2%; Pred. No. 8.8e-31;
Matches 94; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 133 IELTOSPAIMASPGERTVMTCSASSSVRYNWNFQKSGTSPKRWIYDTKLSGVPARF 192
DB 24 IVLTSPIAMSGPGRVTMTCSASSSVSHMHYQKSGTSPKRWIYDTKLSGVPARF 83

QY 193 SGSGSGTGYSLTISMEAEADATYCCQWSSNPLTFGAGTKLELKRAAA 241
DB 84 SGSGSGTGYSLTISNWEAEADATYCHORSSYPWTFGGTKLEIKRADA 132

RESULT 10
Q8K1F2 PRELIMINARY; PRT; 112 AA.
AC Q8K1F2;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Anti-Vipase light chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Hyperimmunized spleen;
RA Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;
RT "Innate proteolytic antibodies: Failed D-Vipase response to the D-
entactinomer of Vip and identification of L-Vipase VL domains.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
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DR EMBL; AF516283; AAM64201.1; -.
DR PIR; H33932; H33932.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SMO0409; IG; 1.
DR SMART; SMO0406; IG; 1.
DR PROSITE; PS00835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 112
FT NON_TER 113
SQ SEQUENCE 112 AA; 11953 MW; 4716887FADBS43ED CRC64;

Query Match 29.6%; Score 480; DB 11; Length 112;
Best Local Similarity 86.4%; Pred. No. 1.2e-30;
Matches 95; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 132 DIETQSPAINASPGERVTWTCASSSVRYMNFQOKSGTSPKRWIYDTSKLSSGVPAR 191
Db 1 DIVLTQSPAINASPGSKVTITCNASSSVSYMHWFQOKPGTSPKLTWYSTNLASGVPAR 60

QY 192 FSGSGSGTSYSLTSSMEADAAATYYCQOWSSNPLTFGAGTKLELKEAA 241
Db 61 FSGSGSGTSYSLTSSMEADAAATYYCQOWSSNPLTFGAGTKLELKEAA 110

RESULT 11
Q9UL90 PRELIMINARY; PRT; 113 AA.
AC Q9UL90
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1
RP MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035024; AAD56260.1; -.
DR HSSP; P01772; 2F84.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SMO0406; IG; 1.
DR PROSITE; PS00835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 113
FT NON_TER 113
SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;

Query Match 28.5%; Score 462.5; DB 4; Length 113;
Best Local Similarity 77.2%; Pred. No. 3e-29;
Matches 88; Conservative 10; Mismatches 15; Indels 1; Gaps 1;

QY 3 EVKLQESGGVLQPGGSKLSCAASGTFSSFGHWHVQAPKGLWAVIISGSGSTIYY 62
Db 1 EVQLVESGGGVQPGGSLRLSCAASGTFSSFGHWHVQAPKGLWAVAFIRYDGSNKYY 60

QY 63 ADTVKGRFTISRDNPNTFLQMTSLRSEDVTMYICARDYCA-----YWGQGTFTVYSS 116
Db 61 ADSVKGRFTISRDNSKNTLYQMNSLRADETAVYCAKDLN-YWGQGLTVYSS 113

RESULT 12
Q8WUK1 PRELIMINARY; PRT; 613 AA.
AC Q8WUK1
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RC Tissue=Tonsil;
RA Straussberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC020240; AAH20240.1; -.
DR PIR; P0120; P0120.
DR PIR; S15590; S15590.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 5.
DR SMART; SMO0406; IG; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
KW Hypothetical protein.
SQ SEQUENCE 613 AA; 67296 MW; 60C7F5950671E315 CRC64;

Query Match 28.5%; Score 462; DB 4; Length 613;
Best Local Similarity 31.3%; Pred. No. 3e-28;
Matches 128; Conservative 46; Mismatches 111; Indels 124; Gaps 11;

QY 3 EVKLQESGGVLQPGGSKLSCAASGTFSSFGHWHVQAPKGLWAVIISGSGSTIYY 62
Db 20 QVQLVESGGGVQPGGSLRLSCAASGTFSSFGHWHVQAPKGLWAVIISGSGNKYY 79

QY 63 ADTVKGRFTISRDNPNTFLQMTSLRSEDVTMYICARDYCA-----YWGQGTFTVYSS 116
Db 80 ADSVKGRFTISRDNSKNTLYQMNSLRADETAVYCAKDLN-YWGQGTFTVYSS 139

QY 117 GGGG-----SGGGSGGG-----GSDIELTQS-PAIM 142
Db 140 GSASAPTLFPLVSCNSPSTSSVAVGCLAQDFLPDSITFSWKYKXNSDISSTRGPPSVL 199

QY 143 SASPGERVMTCSASSV-----
Db 200 RGGKYAATSQVLPSKDVMOGTDEHVCKVQHPNGNKEKVPFLVIAELPKVSVFVPPR 259

QY 161 -----RYMNFQOKSGTSPKR-----WIYDTSKLSSGVPARFSGSGSGTYSLTISME 209
Db 260 DGFFGNPRKSKLIQATGFSRQIQVSWLREGKQVGGV-----TTQVQ 304

QY 210 AEDAATYYCQOWSSNPLTFGAGTKLELKEAAEQKLISEDLNGAVDEQKLISEDLNAV 269
Db 305 AEAK-----ESGPTTYKYVTLTIK-----ESDWLSQSMTCEVDHRLGLTFQGNASSM 352

QY 270 ---GQDTQ-EVIVVPHSLPFKVVVISAILALVLTITSLIILIMLWQKK 314
Db 353 CVPDQDTAIRVFAIPPSFASIFLTKSTKLTCLVTDLTATYSDVTSITWTRQ 401

RESULT 13
Q8KIF3 PRELIMINARY; PRT; 112 AA.
AC Q8KIF3
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-VIPase light chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;

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RN RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Hyperimmunized spleen;
RA Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;
RT "Innate proteolytic antibodies: Failed D-Vipase response to the D-
RL entantlomer of Vip and identification of L-Vipase VL domains.";
DR EMBL; AF516282; AAM64200.1; -.
DR PIR; A33933; A33933.
DR PIR; PH1085; PH1085.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1 112
FT NON_TER 112 112
SQ SEQUENCE 112 AA; 12017 MW; 22DD75B5414CDB18 CRC64;

Query Match 28.4%; Score 461; DB 11; Length 112;
Best Local Similarity 81.8%; Pred. No. 3.9e-29;
Matches 90; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

QY 132 DIETQSPALMSASGPERVTTCASSSVRYNMNPFQKSGTSPKRWIYDTSKLSSGVP 191
DB 1 DIVLTQSPALMSASGPERVTTCASSSVRYNMNPFQKSGTSPKRWIYDTSKLSSGVP 60

QY 192 FSGSGSGTSYSLTISSEAEADAATYYCOQWSSNPLTFCAGTKLEKRAA 241
DB 61 FSGSGSGTSYSLTISSEAEADAATYYCOQWSSNPLTFCAGTKLEKRAA 110

RESULT 14
Q8K1F1 PRELIMINARY; PRT; 114 AA.
AC Q8K1F1
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-Vipase light chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;
RT "Innate proteolytic antibodies: Failed D-Vipase response to the D-
RL entantlomer of Vip and identification of L-Vipase VL domains.";
DR EMBL; AF516284; AAM64202.1; -.
DR PIR; A33933; A33933.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1 114
FT NON_TER 114 114
SQ SEQUENCE 114 AA; 12162 MW; 8BD9833DBF3BEFD1 CRC64;

Query Match 28.2%; Score 458; DB 11; Length 114;
Best Local Similarity 81.2%; Pred. No. 6.9e-29;
Matches 91; Conservative 7; Mismatches 12; Indels 2; Gaps 1;

QY 132 DIETQSPALMSASGPERVTTCASSSV--RYNMNPFQKSGTSPKRWIYDTSKLSSGVP 189
DB 1 DIVLTQSPALMSASGPERVTTCASSSVSSSYLHWYQKSGSPKRWIYDTSKLSSGVP 60

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QY 190 ARFSGSGSGTSYSLTISSEAEADAATYYCOQWSSNPLTFCAGTKLEKRAA 241
DB 61 ARFSGSGSGTSYSLTISSEAEADAATYYCOQWSSNPLTFCAGTKLEKRAA 112

RESULT 15
Q9R1A4 PRELIMINARY; PRT; 437 AA.
AC Q9R1A4
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Gamma heavy chain of Mab7 (Fragment).
GN IGH-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152372; AAD40243.1; -.
DR PIR; B45837; B45837.
DR PDB; 1COK; 11-SEP-99.
DR PDB; 1I31; 25-DEC-02.
DR PDB; 1KCU; 11-MAY-02.
DR MGD; MGI:96446; Igh-4.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 3.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
FT NON_TER 1 437
FT NON_TER 437 437
SQ SEQUENCE 437 AA; 48142 MW; 5C3A7BB3EB7D697C CRC64;

Query Match 28.0%; Score 454.5; DB 11; Length 437;
Best Local Similarity 44.4%; Pred. No. 7.6e-28;
Matches 108; Conservative 23; Mismatches 69; Indels 43; Gaps 7;

QY 4 VKLQESGGGLVQPGGSRKLSCAASGFTFSSFGHWVROAPEKLEWVAYISSGSIYYA 63
DB 1 VQLQESGGGLVQPGGSLKLSCAASGFTFSSYAMSWRQTPKRLWVASFSSG-GIIYIT 59
QY 64 DTVKGRFTISRDNPKNTLFLQNTSLRSBDTVMYYCAR-DYGAYWCGGTVTYVSSGGSGG 122
DB 60 DSVKGRFTIYKDKRNLISLQMSLSRSEDAMYYCARGDYSAWPGTGLVTVSAA----- 114
QY 123 GGGSGGGGSDIELTQSPALMSASGPERVTTCASSSVRYNMNPFQKSGTSPKRWIYDTS 182
DB 115 -----KTPFPSPVPLAPGSAQAQTSNMVTLGCLVKGYPFE-----PVTYWSG 157
QY 183 KLSGGV---PARFSGSGSGTSYSLTISSEAEADAATYYCOQWSSNPLTF-----GAGTKL 234
DB 158 SLSSGVHTFPVLTQSDLYTLSSSVTVPS-----STWPSBTVCNVAHPASSTKV 206
QY 235 ELK 237
DB 207 DXK 209

Search completed: May 27, 2004, 05:58:09
Job time : 52 secs

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OM protein - protein search, using sw model

Run on: May 27, 2004, 05:54:07 ; Search time 60 seconds
(without alignments)
1488.084 Million cell updates/sec

Title: US-09-403-882A-2

Perfect score: 1622

Sequence: 1 MAEVKIQESGGLVQPGGR.....VLTITSLILMLWQKKPR 316

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_29Jan04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1622	100.0	316	2	AAY32086 Single ch
2	1319	81.3	255	3	AAB11398 E. coli e
3	1319	81.3	255	4	AAB74199 PelB-scfv
4	1319	81.3	255	4	AAB70769 Expressio
5	1319	81.3	255	4	AAY72020 E. caroto
6	1237	76.3	241	6	ABr62010 Single-ch
7	1227	75.6	241	5	AAM48925 scFv anti
8	1194	73.1	236	2	AAR32842 VH NQ10/1
9	1185	73.1	240	2	AAR32841 Single ch
10	1097	67.7	223	2	AAR32841 VH NQ10/1
11	1008	62.1	580	2	AAY90217 Bispecifi
12	1001	61.7	556	2	AAR90218 Bispecifi
13	976.5	60.2	237	7	AAR38657 Mouse G1
14	970.5	59.8	268	3	AAY44973 Recombina
15	967.5	59.6	268	3	AAY44972
16	964.5	59.5	284	2	AAR95569 Intracell
17	954	58.8	280	6	ABR42055 Newcastl
18	939	57.3	234	2	AAR64819 OMVU10 Sc
19	938.5	57.9	235	2	AAR32840 VH NQ2/12
20	937	57.8	258	2	AAR90221 Anti-B7.1
21	935.5	57.7	294	4	AB20442 Anti-FIX/
22	934.5	57.6	293	4	AB20441 Amino aci
23	928.5	57.2	282	6	ABJ19276 Anti-huma
24	919	56.7	553	2	AAR11508 Single ch
25	919	56.7	553	2	AAR73223 H22-anti-

26	919	56.7	553	4	ABR61960
27	919	56.7	553	4	ABR85455
28	913	56.3	242	6	ABR62132 Single ch
29	907	55.9	353	2	AAY06273 Anti Fc a
30	906.5	55.9	237	5	ABP46093 Human BLY
31	906.5	55.9	253	2	AAW90225 Anti-B7.1
32	903.5	55.7	237	5	ABP46009 Human BLY
33	900.5	55.5	237	5	ABP46103 Human BLY
34	900.5	55.5	237	5	ABP45994 Human BLY
35	900.5	55.5	281	2	AAW82744 Fusion pr
36	899.5	55.5	237	5	ABP46107 Human BLY
37	898.5	55.4	237	5	ABP46104 Human BLY
38	897.5	55.3	237	5	ABP46100 Human BLY
39	897.5	55.3	237	5	ABP46016 Human BLY
40	897.5	55.3	245	2	AAW06717 Antibody
41	897.5	55.3	503	5	AAU72874 3B10xP5-2
42	897	55.3	239	2	AAU17963 Mouse scf
43	897	55.3	256	5	AAU72866 P5-3 sing
44	896.5	55.3	237	5	ABP46017 Human BLY
45	896.5	55.3	237	5	ABP45992 Human BLY

ALIGNMENTS

RESULT 1

AAV32086

ID AAV32086 standard; protein; 316 AA.

AC AAY32086;

DT 17-JAN-2000 (first entry)

DE Single chain antibody used in probe detection.

DX Single chain antibody; scAb; sfv; spectroscopic probe.

OS Unidentified.

PN WO9951986-A1.

PD 14-OCT-1999.

PF 08-APR-1999; 99WO-US007847.

PR 08-APR-1998; 98US-0081118P.

PR 09-APR-1998; 98US-0081340P.

XX (REGC) UNIV CALIFORNIA.

XX Farinas J;

XX WPI; 1999-611066/52.

XX N-PSDB; AAZ20266.

Localizing probes to specific sites in cells that express single-chain antibody reactive with probe-ligand conjugate, particularly for detecting post-translational modification and its modulators.

Claim 5; Page 47-48; 69pp; English.

The present sequence represents a single chain antibody (scAb) that has 2 c-myc epitopes. The scAb is used in claimed methods for localizing a probe and for detecting a post-translational activity in a cell, and is expressed by a claimed transgenic non-human animal. The invention provides methods and reagents for targeting probes to selected cellular locations through the expression of specific binding partners (such as scAbs) within a cell, and for creating assays for post-translational activities. The invention allows the monitoring of the location of such intracellular, specific binding partners over time and in response to stimuli, such as test chemicals. Spectroscopic probes can be used to screen a test chemical for activity. The invention also includes cells and transgenic organisms comprising the intracellular specific binding

CC partner, where the specific binding partner can bind with the
 CC spectroscopic probe/ligand conjugate, scbbs can be expressed within the
 CC cell and can be designed to bind a wide variety of spectroscopic probes,
 CC including small molecules that have better (and more diverse)
 CC spectroscopic properties than green fluorescent protein
 XX
 SQ Sequence 316 AA;

Query Match 100.0%; Score 1622; DB 2; Length 316;
 Best Local Similarity 100.0%; Pred. No. 2e-108;
 Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAEVKLQSGGGLVQPGGSRKLSCAASGFTFSFGMHVVRQAPKGLWVAYISSGSSTI 60
 DB 1 MAEVKLQSGGGLVQPGGSRKLSCAASGFTFSFGMHVVRQAPKGLWVAYISSGSSTI 60
 QY 61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDVWYICARDYGAYWGCGTTVTSSGGGG 120
 DB 61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDVWYICARDYGAYWGCGTTVTSSGGGG 120
 QY 121 SGGGSGGGGSDIELTQSPAIMSASPGERVMTWTCASSSVRYMNVFQKSGTSPKRWIYD 180
 DB 121 SGGGSGGGGSDIELTQSPAIMSASPGERVMTWTCASSSVRYMNVFQKSGTSPKRWIYD 180
 QY 181 TSKLSSGVPARFSGSGGTSYSLTISSEAEADAATYICQWSSNPLTFGAGTKLELKRAA 240
 DB 181 TSKLSSGVPARFSGSGGTSYSLTISSEAEADAATYICQWSSNPLTFGAGTKLELKRAA 240
 QY 241 AEQKLISEEDLNGADEVQKLSIEDLNAVGDQTOEVIWPHSLPFKVVVISAILALVLT 300
 DB 241 AEQKLISEEDLNGADEVQKLSIEDLNAVGDQTOEVIWPHSLPFKVVVISAILALVLT 300
 QY 301 IISLIILMLWQKKPR 316
 DB 301 IISLIILMLWQKKPR 316

RESULT 2

AAB11398
 ID AAB11398 standard; protein; 255 AA.
 AC AAB11398;
 DT 22-FEB-2001 (first entry)
 DE E. coli expression plasmid pUBS520-ScFvOx encoded protein.
 XX
 KW Eukaryotic protein; protease; interferon; antibody; hormone;
 KW disulfide bridge.
 XX Escherichia coli.
 OS Synthetic.
 XX
 PN EP1048732-A1.
 PD 02-NOV-2000.
 PF 26-APR-1999; 99EP-00107412.
 PR 26-APR-1999; 99EP-00107412.
 XX
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX
 DR WPI; 2000-674185/66.
 DR N-PSDB; AAC65074.
 XX
 PT Preparation of water-soluble eukaryotic polypeptides with disulfide
 PT bridges e.g. rPA, comprises cultivation of prokaryotic cells in the
 PT presence of arginine or amide compound.
 XX
 PS Example 6; Page 22-23; 40pp; German.
 XX
 CC This invention describes a novel preparation of a water-soluble,

CC naturally occurring eukaryotic polypeptide containing two or more
 CC cysteine units bound via a disulfide bridge which comprises cultivation
 CC of prokaryotic cells in the presence of arginine or an amide compound.
 CC The method is useful for the preparation of eukaryotic proteins e.g.
 CC proteases, interferons, protein hormones, antibodies or antibody
 CC fragments (e.g. a single chain FV fragment that binds to thyroid
 CC stimulating hormone). It is especially useful for preparing proteins with
 CC more than five disulfide bridges, e.g. recombinant plasminogen activator
 CC (rPA). the technique is simple and does not require in vitro after-
 CC treatment, such as the removal of inclusion bodies, reduction or
 CC nitrization
 XX

SQ Sequence 255 AA;

Query Match 81.3%; Score 1319; DB 3; Length 255;
 Best Local Similarity 99.2%; Pred. No. 8.8e-87;
 Matches 252; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MAEVKLQSGGGLVQPGGSRKLSCAASGFTFSFGMHVVRQAPKGLWVAYISSGSSTI 60
 DB 1 MAEVKLQSGGGLVQPGGSRKLSCAASGFTFSFGMHVVRQAPKGLWVAYISSGSSTI 60
 QY 61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDVWYICARDYGAYWGCGTTVTSSGGGG 120
 DB 61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDVWYICARDYGAYWGCGTTVTSSGGGG 120
 QY 121 SGGGSGGGGSDIELTQSPAIMSASPGERVMTWTCASSSVRYMNVFQKSGTSPKRWIYD 180
 DB 121 SGGGSGGGGSDIELTQSPAIMSASPGERVMTWTCASSSVRYMNVFQKSGTSPKRWIYD 180
 QY 181 TSKLSSGVPARFSGSGGTSYSLTISSEAEADAATYICQWSSNPLTFGAGTKLELKRAA 240
 DB 181 TSKLSSGVPARFSGSGGTSYSLTISSEAEADAATYICQWSSNPLTFGAGTKLELKRAA 240
 QY 241 AEQKLISEEDLNGA 254
 DB 241 AEQKLISEEDLNGA 254

RESULT 3

AAB74199
 ID AAB74199 standard; protein; 255 AA.
 AC AAB74199;
 DT 29-MAY-2001 (first entry)
 DE PelB-scFvOxazolon fusion protein.
 XX
 KW Molecular chaperone; PelB signal sequence; scFvOxazolon.
 XX
 OS Unidentified.
 XX
 PN EP1077262-A1.
 PD 21-FEB-2001.
 PF 24-JUL-2000; 2000EP-00115839.
 PR 29-JUL-1999; 99EP-00114811.
 XX
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX
 PI Ambrosius D, Rudolph R, Schaeffner J, Schwarz E;
 XX
 DR WPI; 2001-246712/26.
 DR N-PSDB; AAF77806.
 XX
 PT Producing naturally folded eukaryotic proteins e.g. antibodies,
 PT interferon, hormones or proteases that contain two or several cysteines
 PT linked by disulfide bridges comprises co-expression of a molecular
 PT chaperone.
 XX

PS Disclosure; Page 19; 35pp; English.

XX The present invention relates to a method for production of a naturally
 CC folded eukaryotic protein containing two or more cysteines linked by
 CC disulfide bridges. The method comprises co-expression and secretion into
 CC the periplasm of a molecular chaperone via an expression vector coding
 CC for the chaperone. The expression vector also encodes a signal sequence.
 CC The method is useful for producing a naturally folded eukaryotic protein
 CC such as an antibody, antibody fragment, interferon, protein hormone or a
 CC protease containing two or several cysteines linked by disulfide bridges.
 CC The present sequence is a fusion protein composed of the PelB signal
 CC sequence and ScFvOxazolon. This sequence was used in the method of the
 CC present invention

XX SQ Sequence 255 AA;

Query Match 81.3%; Score 1319; DB 4; Length 255;
 Best Local Similarity 99.2%; Pred. No. 8.8e-87;
 Matches 252; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAEVKLOESGGGLVQPGGSRKLSCAASGFTFSFGHWHVWVQAPEKGLEWVAYISSGSTI 60
 DB 1 MAEVKLOESGGGLVQPGGSRKLSCAASGFTFSFGHWHVWVQAPEKGLEWVAYISSGSTI 60

QY 61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDVVMYICARDYCAWYGGQTTTVSSGGGG 120
 DB 61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDVVMYICARDYCAWYGGQTTTVSSGGGG 120

QY 121 SGCGGGGGGSDIELTQSPAIMSASGERVTMTCSASSSVRYMNVFQOKSGTSPKRWIYD 180
 DB 121 SGCGGGGGGSDIELTQSPAIMSASGERVTMTCSASSSVRYMNVFQOKSGTSPKRWIYD 180

QY 181 TSKLSSGVPARFSGSGSGTYSYLTSSMEADAATYYCQWSSNPLTFGAGTKLELRAA 240
 DB 181 TSKLSSGVPARFSGSGSGTYSYLTSSMEADAATYYCQWSSNPLTFGAGTKLELRAA 240

QY 241 AEOKLISEEDLNGA 254
 DB 241 AEOKLISEEDLNGA 254

RESULT 4
 AAB70769
 ID AAB70769 standard; protein; 255 AA.
 AC AAB70769;
 DT 18-MAY-2001 (first entry)
 XX Expression plasmid pUBS520-ScFvOx protein.
 DE Chaperone protein; periplasm; antibody production; protein production;
 KW interferon production; protease production.
 XX Escherichia coli.
 OS Synthetic.
 XX EP1077263-A1.
 XX EP1077263-A1.
 XX 21-FEB-2001.
 XX 29-JUL-1999; 99EP-00114811.
 XX 29-JUL-1999; 99EP-00114811.
 XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX WPI: 2001-204356/21.
 XX N-PSDB; AAF61193.
 XX Preparation of naturally folded eukaryotic proteins, e.g. antibodies, by
 PT simultaneous expression of a chaperone protein, allows simple recovery
 PT from periplasm or medium.

XX PS Disclosure; Page 20-21; 36pp; German.

XX This invention describes a novel method for preparing a naturally folded
 CC eukaryotic polypeptide (I) that contains two or more disulfide-bridged
 CC Cys residues by culturing prokaryotic cells that contain an expression
 CC vector for (I) including a prokaryotic signal sequence at its N-terminus
 CC and a nucleic acid (II) that secretes a chaperone protein (III) into the
 CC periplasm. (I) is secreted into the periplasm or medium; the signal
 CC peptide is then cleaved and (I) isolated from the periplasm or medium.
 CC The method is used for production of antibody, interferon, protein
 CC hormone or protease. Expression of (III) increases the yield of (I). The
 CC method is simple and eliminates time-consuming in vitro processing
 CC operations such as dissolution of inclusion bodies, reduction and
 CC refolding. (III) protects (I) against agglomeration and promotes their
 CC natural conformation

XX SQ Sequence 255 AA;

Query Match 81.3%; Score 1319; DB 4; Length 255;
 Best Local Similarity 99.2%; Pred. No. 8.8e-87;
 Matches 252; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAEVKLOESGGGLVQPGGSRKLSCAASGFTFSFGHWHVWVQAPEKGLEWVAYISSGSTI 60
 DB 1 MAEVKLOESGGGLVQPGGSRKLSCAASGFTFSFGHWHVWVQAPEKGLEWVAYISSGSTI 60

QY 61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDVVMYICARDYCAWYGGQTTTVSSGGGG 120
 DB 61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDVVMYICARDYCAWYGGQTTTVSSGGGG 120

QY 121 SGCGGGGGGSDIELTQSPAIMSASGERVTMTCSASSSVRYMNVFQOKSGTSPKRWIYD 180
 DB 121 SGCGGGGGGSDIELTQSPAIMSASGERVTMTCSASSSVRYMNVFQOKSGTSPKRWIYD 180

QY 181 TSKLSSGVPARFSGSGSGTYSYLTSSMEADAATYYCQWSSNPLTFGAGTKLELRAA 240
 DB 181 TSKLSSGVPARFSGSGSGTYSYLTSSMEADAATYYCQWSSNPLTFGAGTKLELRAA 240

QY 241 AEOKLISEEDLNGA 254
 DB 241 AEOKLISEEDLNGA 254

RESULT 5
 AAY72020
 ID AAY72020 standard; protein; 255 AA.
 AC AAY72020;
 DT 28-MAR-2001 (first entry)
 XX E. carotovora PelB-scfVox fusion protein encoded by pUBS520-pIN-scfVox.
 DE Secreted protein; chaperone; interferon; protease; hormone;
 KW naturally folded protein; lac promoter; DnaJ; heat shock protein; HSP;
 KW pectate lyase B; PelB; hapten; single-chain Fv-fragment Oxazolon;
 KW scFvOxazolon; fusion protein; thyroid stimulating hormone; TSH.
 XX Pectobacterium carotovorum.
 OS Unidentified.
 OS Chimeric.
 XX EP1054063-A2.
 XX 22-NOV-2000.
 XX 19-APR-2000; 2000EP-00108505.
 XX 26-APR-1999; 99EP-00107412.
 XX (HOFF) HOFFMANN LA ROCHE & CO AG F.

PI Ambrosius D, Rudolph R, Schaeffner J, Schwarz E;
 XX WPI; 2001-033777/05.
 DR N-PSDB; AAD02212.
 XX
 PT Producing water-soluble, naturally folded, and secreted eukaryotic
 PT polypeptide, involves culturing prokaryotic cells containing an
 PT expression vector encoding the polypeptide in the presence of arginine or
 PT a specific compound.
 XX
 PS Example 6; Page 22-23; 35pp; English.

XX The patent discloses a method for the production of a water-soluble,
 CC naturally folded and secreted eukaryotic proteins in prokaryotic cells.
 CC The method involves culturing the prokaryotic cells, containing an
 CC expression vector encoding the desired protein and the prokaryotic signal
 CC sequence, in the presence of an additive, e.g., L-arginine. The signal
 CC sequence mediates the secretion of the desired protein into the
 CC periplasm, where folding of the protein takes place. The prokaryotic cell
 CC also contains an expression vector encoding a molecular chaperone, e.g.,
 CC DnaJ and heat shock protein 25 (HSP25). The simultaneous co-
 CC overexpression and co-secretion of molecular chaperones in the periplasm
 CC improves the yield of functionally folded protein. The above method
 CC recombinantly produces a high yield of eukaryotic secreted proteins in
 CC prokaryotes. The method is useful for producing eukaryotic proteins such
 CC as an antibody, antibody fragment, interferon, protein hormone or a
 CC protease. The present sequence is an Erwinia carotovora pectate lyase B
 CC (PelB) signal sequence-scFvOx fusion protein encoded by PUBS520-pIN-
 CC scFvOx. The plasmid, PUBS520-pIN-scFvOx, also comprises the lac promoter.
 CC The single-chain Fv-fragment, which is directed against the haptan
 CC oxazolone (scFvOxazolone), is an antibody fragment against thyroid
 CC stimulating hormone (TSH). The co-expression of scFvOx which has no
 CC chaperone properties is used as a negative control
 XX Sequence 255 AA;

Query Match 81.3%; Score 1319; DB 4; Length 255;
 Best Local Similarity 99.2%; Pred. No. 8.8e-87;
 Matches 252; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MAEVLQESGGGLVQPGGSRKLSCAASGFTFSFGMHWVRQAPKGLWVAYISSGSSTI 60
 Db 1 MAEVLQESGGGLVQPGGSRKLSCAASGFTFSFGMHWVRQAPKGLWVAYISSGSSTI 60
 QY 61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYICARDYGYWQGGTTVTYSSGGGG 120
 Db 61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYICARDYGYWQGGTTVTYSSGGGG 120
 QY 121 SGGGGGGGGSDIELTQSPAIMSASPGERVMTCSASSSVRYMNFQKSGTSPKRWIYD 180
 Db 121 SGGGGGGGGSDIELTQSPAIMSASPGERVMTCSASSSVRYMNFQKSGTSPKRWIYD 180
 QY 181 TSKLSSGVPARFSGSGSGTSYSLTISSEAEADAATYCCQWSSNPLTFGAGTKLELKRAA 240
 Db 181 TSKLSSGVPARFSGSGSGTSYSLTISSEAEADAATYCCQWSSNPLTFGAGTKLELKRAA 240
 QY 241 AEQKLISEEDLNGA 254
 Db 241 AEQKLISEEDLNGA 254

RESULT 6
 ABR62010
 ID ABR62010 standard; protein; 241 AA.
 XX
 AC ABR62010;
 XX
 XX
 DT 03-OCT-2003 (first entry)
 DE Single-chain (scFv) antibody.
 XX
 XX Transgenic; biomolecule; ATP; ADP; cytosstatic; virucide; gene therapy;
 XX antisense therapy; scFv; antibody.

XX Synthetic.
 XX EP1321524-A1.
 XX
 PD 25-JUN-2003.
 XX
 XX 19-DEC-2001; 2001EP-00130319.
 PF
 XX 19-DEC-2001; 2001EP-00130319.
 PR
 XX (DUEP/) DUERING K.
 PA
 XX Mahn A, Hantke S, Petsch D;
 PI WPI; 2003-543829/52.
 DR N-PSDB; ACC84876.
 XX
 XX Increasing the content of transgene-coded biomolecules in a plant or
 PT animal, useful for producing proteins for diagnosing, preventing and/or
 PT treating viral diseases and cancer, comprises changing the distribution
 PT of ATP and/or ADP.
 XX
 XX Example 2; Fig 2; 18pp; English.

XX The invention relates to increasing the content of one or more transgene-
 CC coded biomolecules in an organism and involves changing the distribution
 CC of ATP and/or ADP in cells of the organism. The yield of transgenic
 CC molecules in host cells is often insufficient for industrial production.
 CC The method increases the yield of transgenic molecules in animal and
 CC plant host cells, therefore facilitating their production on an
 CC industrial scale. The proteins produced by the method are useful for
 CC diagnosing, preventing and/or treating viral diseases and cancer. The
 CC present sequence represents a single-chain (scFv) antibody, used to
 CC exemplify the increase in the expression of scFv antibodies in transgenic
 CC potato tubers
 XX

Query Match 76.3%; Score 1237; DB 6; Length 241;
 Best Local Similarity 97.9%; Pred. No. 6.3e-81;
 Matches 235; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 2 AEVLQESGGGLVQPGGSRKLSCAASGFTFSFGMHWVRQAPKGLWVAYISSGSSTIY 61
 Db 2 AEVLQESGGGLVQPGGSRKLSCAASGFTFSFGMHWVRQAPKGLWVAYISSGSSTIY 61
 QY 62 YADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYICARDYGYWQGGTTVTYSSGGGG 121
 Db 62 YADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYICARDYGYWQGGTTVTYSSGGGG 121
 QY 122 GGGGGGGGGSDIELTQSPAIMSASPGERVMTCSASSSVRYMNFQKSGTSPKRWIYD 181
 Db 122 GGGGGGGGGSDIELTQSPAIMSASPGERVMTCSASSSVRYMNFQKSGTSPKRWIYD 181
 QY 182 SKLSSGVPARFSGSGSGTSYSLTISSEAEADAATYCCQWSSNPLTFGAGTKLELKRAA 241
 Db 182 SKLSSGVPARFSGSGSGTSYSLTISSEAEADAATYCCQWSSNPLTFGAGTKLELKRAA 241

RESULT 7
 AAM48925
 ID AAM48925 standard; protein; 241 AA.
 XX
 AC AAM48925;
 XX
 DT 03-MAY-2002 (first entry)
 DE scFv antibody.
 XX
 XX Ketone binding protein; oxazole; pathogen resistance; virucide;
 XX fungicide; antibacterial; scFv antibody.

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OS XX Unidentified.
PH XX
FT XX Key Location/Qualifiers
FT XX Misc-difference 137 /note= "encoded by CAG"
FT XX Misc-difference 201 /note= "encoded by TAC"
XX XX
XX XX WO200204020-A2.
XX XX
XX XX 17-JAN-2002.
XX XX
XX XX 17-MAY-2001; 2001WO-DE001916.
XX XX
XX XX 12-JUL-2000; 2000DE-01033750.
XX XX
XX XX (NPBC-) MPB COLOGNE GMBH.
XX XX
XX XX Duerling K, Brinkmann O;
XX XX
XX XX WPI; 2002-154868/20.
XX XX N-PSDB; AAK98639.
XX XX
XX XX Imparting pathogen resistance to plants and animals, comprises using a
XX XX polypeptide that binds to an oxazole-derived ketone, optionally expressed
XX XX from nucleic acid.
XX XX
XX XX Example 3; Fig 1; 20pp; German.
XX XX
XX XX The present invention relates to the use of a polypeptide that binds a
XX XX ketone derived from oxazole for generating pathogen resistance in an
XX XX organism. This can be used to impart resistance to pathogens (bacteria,
XX XX fungi or viruses) to a wide range of plants (e.g. cereals, sugar beet,
XX XX tobacco etc.), humans, farm animals and pets. Exemplified are activities
XX XX against Phytophthora infestans and Erwinia carotovora in potatoes and
XX XX Staphylococcus aureus in mice. The present sequence is a sc-Fv antibody,
XX XX which is capable of binding 2-phenyloxazol-5-one
XX XX
XX XX Sequence 241 AA;
XX XX
XX XX Query Match 75.6%; Score 1227; DB 5; Length 241;
XX XX Best Local Similarity 97.1%; Pred. No. 3.3e-80;
XX XX Matches 234; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
XX XX
QY 1 MAEVLQESGGGLVQPGGSRKLSCAASGFTFSSFGHWWVROAPEKGLWVAYISSGSTI 60
DB 1 MADVLVESGGGLVQPGGSRKLSCAASGFTFSSFGHWWVROAPEKGLWVAYISSGSTI 60
QY 61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYICARDYGATGAGTGTVTYSSGGG 120
DB 61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYICARDYGATGAGTGTVTYSSGGG 120
QY 121 SGGGGSGGGSDIELTQSPAIMSAPGKVTMTCSASSVRVYMWVFOQKSGTSPKRWIYD 180
DB 121 SGGGGSGGGSDIELTQSPAIMSAPGKVTMTCSASSVRVYMWVFOQKSGTSPKRWIYD 180
QY 181 TSKLSSGVPARSGSGSGTSTYSLTSSMEADAATYTCQWSSNPLTFCAGTKLEKRAA 240
DB 181 TSKLSSGVPARSGSGSGTSTYSLTSSMEADAATYTCQWSSNPLTFCAGTKLEKRAA 240
QY 241 A 241
DB 241 A 241
XX XX
XX XX RESULT 8
XX XX AAR32842
XX XX ID AAR32842 standard; protein; 236 AA.
XX XX
XX XX AAR32842;
XX XX
XX XX 25-MAR-2003 (revised)
XX XX 19-JUN-1993 (first entry)

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XX XX VH NQ10/12.5-Vk NQ10/12.5 linked peptide sequences #2.
XX XX
XX XX Primer; human; immunoglobulin; Ig; variable region; VH; VL; Ck; JH;
XX XX lymphocyte; vector; soluble; antibody; phage; linker; back; VH3; restated;
XX XX in-cell PCR; cloning; polymorphic; TCR V; anti-phenyloxazolone; hybridoma;
XX XX NQ2/12.4; NQ10/12.5.
XX XX
XX XX Synthetic.
XX XX
XX XX Key Location/Qualifiers
XX XX Region 1..115
XX XX /label= VH_NQ10/12.5
XX XX Peptide 116..129
XX XX /note= "Linker peptide"
XX XX Region 130..236
XX XX /label= Vkappa_NQ10/12.5
XX XX
XX XX WO9303151-A1.
XX XX 18-FEB-1993.
XX XX
XX XX 10-AUG-1992; 92WO-GB001483.
XX XX
XX XX 10-AUG-1991; 91GB-00017352.
XX XX 11-JUN-1992; 92GB-00012419.
XX XX
XX XX (MEDI-) MEDICAL RES COUNCIL.
XX XX
XX XX Embleton MJ, Gorochov G, Jones PT, Winter GP;
XX XX WPI; 1993-076508/09.
XX XX N-PSDB; AAQ37461.
XX XX
XX XX Treatment of cell populations, partic. hybridomas - to link together
XX XX copies of 2 or more non-contiguous DNA sequences to facilitate analysis.
XX XX
XX XX Disclosure; Fig 4; 72pp; English.
XX XX
XX XX The sequences given in AAR32840-43 show the mature heavy chain VH domains
XX XX and the VK light chain genes of the anti-phenyloxazolone hybridomas
XX XX NQ2/12.4 and NQ10/12.5 which have been linked via a linker peptide by in-
XX XX cell PCR. The cDNA encoding these peptides was synthesised using forward
XX XX primers annealing to the Ck gene and the JH segment, followed by assembly
XX XX with linker primers, VH back primers based on the VH3 leader sequence and
XX XX a forward Ck primer, nested in respect to the primer used for cDNA. The
XX XX assembled product within the cells is then amplified with nested primers
XX XX annealing to the 5' end of the VH gene and the 3' end of the Jk segment.
XX XX In-cell PCR may be used to determine gene linkage analysis, particularly
XX XX for the cloning of gene combinations that are polymorphic within a
XX XX population of cells, such as the rearranged genes for Ig or TCR V
XX XX regions. (Updated on 25-MAR-2003 to correct FN field.)
XX XX
XX XX Sequence 236 AA;
XX XX
XX XX Query Match 73.6%; Score 1194; DB 2; Length 236;
XX XX Best Local Similarity 96.2%; Pred. No. 7.5e-78;
XX XX Matches 226; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
XX XX
QY 3 EVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGHWWVROAPEKGLWVAYISSGSTIY 62
DB 1 DVQLVESGGGLVQPGGSRKLSCAASGFTFSSFGHWWVROAPEKGLWVAYISSGSTIY 60
QY 63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYICARDYGATGAGTGTVTYSSGGGG 122
DB 61 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYICARDYGATGAGTGTVTYSSGGGG 120
QY 123 GGGSGGGSDIELTQSPAIMSAPGKVTMTCSASSVRVYMWVFOQKSGTSPKRWIYD 182
DB 121 GGGSGGGSDIELTQSPAIMSAPGKVTMTCSASSVRVYMWVFOQKSGTSPKRWIYD 180
QY 183 KLSGGVPARESGSGSGTSTYSLTSSMEADAATYTCQWSSNPLTFCAGTKLEK 237

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Query Match 67.7%; Score 1097.5; DB 2; Length 223;
 Best Local Similarity 90.2%; Pred. No. 5.9e-71;
 Matches 212; Conservative 4; Mismatches 6; Indels 13; Gaps 1;

QY 3 EVKLQESGGGLVQPGGSRKLSCAASGFTFSFGHVRQAPKGLWVAYISGSGSTIYY 62
 DB 1 DVQLVESGGGLVQPGGSRKLSCAASGFTFSFGHVRQAPKGLWVAYISGSGSTIYY 60

QY 63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDVYMYCARDYAGVWGQTTVYSSGGSGG 122
 DB 61 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDVYMYCARDYAGVWGQTTVYSSA----- 114

QY 123 GGGSGGGSDIELTQSPAIMSASGERVTWTCSSASSVRVMWFOQKSGTSPKRWLYDTS 182
 DB 115 -----ASQIVLTQSPAIMSASGERVTWTCSSASSVRVMWFOQKSGTSPKRWLYDTS 167

QY 183 KLSGVPARTSGSGSTYSGLTSSMEADAATYYCQWSSNPLTFGAGTKLELK 237
 DB 168 KLSGVPARTSGSGSTYSGLTSSMEADAATYYCQWSSNPLTFGAGTKLELK 222

RESULT 11
 AAW90217
 ID AAW90217 standard; protein; 580 AA.
 AC AAW90217;
 XX
 DT 10-MAY-1999 (first entry)
 XX
 DE Bispecific tetraivalent antibody BitAbB7-24-IG10H6.
 XX
 KW B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2; CD86;
 KW T cell activation; inhibitor; graft versus host disease;
 KW transplant rejection; allograft rejection; autoimmune disease; allergy;
 KW therapy; human; bispecific tetraivalent antibody; BitAb;
 KW BitAbB7-24-IG10H6.
 XX
 OS Mus sp.
 OS Homo sapiens.
 OS Synthetic.
 OS Chimeric.
 XX

Key Location/Qualifiers
 FT Peptide 1..224
 FT /note= "pe1b signal peptide"
 FT Region 25..138
 FT /note= "VH region anti B7.1 Mab"
 FT Peptide 139..153
 FT /note= "(G4S3) flexible linker"
 FT Region 154..262
 FT /note= "VL region anti B7.1 Mab"
 FT Misc-difference 261
 FT /note= "encoded by CTG"
 FT Region 263..273
 FT /note= "human IgG3 hinge region"
 FT Domain 274..308
 FT /note= "helix-turn-helix dimerisation domain"
 FT Domain 309..319
 FT /note= "human IgG3 hinge domain"
 FT Region 320..446
 FT /note= "VH region anti B7.2 Mab"
 FT Misc-difference 322..327
 FT /note= "codons for these amino acids are not present in the DNA sequence for BitAbB7-24-IG1-H6 provided in the specification"
 FT Peptide 447..461
 FT /note= "(G4S3)flexible linker"
 FT Region 462..574
 FT /note= "VL region anti B7.2 Mab"
 FT Peptide 575..580
 FT /note= "His6 tag"
 XX

PN WO9858965-A2.
 XX 30-DEC-1998.
 XX
 PF 22-JUN-1998; 98WO-EP003791.
 XX
 PR 20-JUN-1997; 97EP-00870092.
 XX
 PA (INNO-) INNOGENETICS NV.
 XX
 PI Lorre K, Sablon E, Buyse M, Bosman A;
 XX WPI; 1999-105615/09.
 DR N-PSDB; AAX01651.
 XX
 PT New molecules which bind B7.1 and B7.2 - useful to prevent and treat
 XX immune diseases including allograft rejection.
 PS Example 7.1; Fig 16; 182pp; English.
 XX
 CC This polypeptide comprises the bispecific tetraivalent antibody BitAbB7-24
 CC -IG10H6. The molecule consists of 4 scFvs, i.e. 2 anti B7.1 scFvs and 2
 CC anti B7.2 scFvs (tetravalency). One single BitAb is a homodimer of 2
 CC identical molecules, each containing both an anti B7.1 and anti B7.2 scFv
 CC (bispecificity). An anti-B7.1 and anti-B7.2 scFv are linked using a
 CC dimerisation domain (see AAW90219), which drives the homodimerisation of
 CC the molecule. DNA (see AAX01651) encoding the BitAb has been constructed
 CC to allow expression of the BitAb in transformed E. coli cells. The BitAb
 CC cross-links, and/or cross-reacts, with the costimulatory molecules B7.1
 CC and B7.2 that are expressed on the membrane of professional antigen-
 CC presenting cells, leading to the inhibition of antigen-specific T cell
 CC activation. The invention relates to such B7-binding molecules, methods
 CC for their production, and their use for treating or preventing diseases
 CC of the immune system, in particular graft rejection, graft versus host
 CC disease, allergy and autoimmune diseases (claimed)
 XX
 SQ Sequence 580 AA;

Query Match 62.1%; Score 1008; DB 2; Length 580;
 Best Local Similarity 80.2%; Pred. No. 4.8e-64;
 Matches 194; Conservative 19; Mismatches 25; Indels 4; Gaps 2;

QY 1 MAEVKLBESGGGLVQPGGSRKLSCAASGFTFSFGHVRQAPKGLWVAYISGSGSTI 60
 DB 21 MAQVQLQESGGGLVQPGGSRRLSCAASGFTFSFGHVRQAPKGLWVAFISVSSTLI 80

QY 61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDVYMYCARD--YGAYWGQTTVYSSGG 118
 DB 81 YYADSVKGRFTISRDNPKNTLFLQMTSLRSEDVYMYCARDGWYFDYWGQTTVYSSGG 140

QY 119 GSGGGGGGGGGSDIELTQSPAIMSASGERVTWTCSSASSVRVM--WFOQKSGTSPKR 176
 DB 141 GSGGGGGGGGGSDIELTQSPSSMAASGVRVTITCVSSRISNLHWYQOKSETSPKP 200

QY 177 WIYDTSKLSSGVAPRPSGSGSTYSGLTSSMEADAATYYCQWSSNPLTFGAGTKLEL 236
 DB 201 WIYDTSNLAGVPRPSGSGSTYDITLTSSMQPEDAATYYCQWSSYPLTFGQGTLEI 260

QY 237 KR 238
 DB 261 KR 262

RESULT 12
 AAW90218
 ID AAW90218 standard; protein; 556 AA.
 XX
 AC AAW90218;
 XX
 DT 10-MAY-1999 (first entry)
 XX
 DE Bispecific tetraivalent antibody BitAb1G10-B7-24H6.
 XX

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 27, 2004, 05:56:57 ; Search time 750 Seconds
(without alignments)
117.657 Million cell updates/sec

Title: US-09-403-882A-2

Perfect score: 1622

Sequence: 1 MAEVLQESGGGLVPGGSR.....VLTIIISLIILMLWQKKR 316

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1151071 seqs, 279249464 residues

Total number of hits satisfying chosen parameters: 1151071

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09D_PUBCOMB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	959	59.1	291	12	US-10-406-830-10
2	943.5	58.2	288	9	US-09-818-247-22
3	927	57.2	291	12	US-10-406-830-9
4	926	57.1	287	12	US-10-406-830-5
5	913	56.3	242	14	US-10-259-087A-20
6	906.5	55.9	237	10	US-09-880-748-2104
7	906.5	55.9	237	12	US-10-293-418-2104
8	903.5	55.7	237	10	US-09-880-748-2020
9	903.5	55.7	237	12	US-10-293-418-2020
10	900.5	55.5	237	10	US-09-880-748-2005
11	900.5	55.5	237	10	US-09-880-748-2114
12	900.5	55.5	237	12	US-10-293-418-2005
13	900.5	55.5	237	12	US-10-293-418-2114
14	899.5	55.5	237	10	US-09-880-748-2118
15	899.5	55.5	237	12	US-10-293-418-2118

16	898.5	55.4	237	10	US-09-880-748-2115
17	898.5	55.4	237	12	US-10-293-418-2115
18	897.5	55.3	237	10	US-09-880-748-2027
19	897.5	55.3	237	10	US-09-880-748-2111
20	897.5	55.3	237	12	US-10-293-418-2027
21	897.5	55.3	237	12	US-10-293-418-2111
22	897.5	55.3	503	12	US-10-239-656-77
23	897	55.3	256	12	US-10-239-656-61
24	896.5	55.3	237	10	US-09-880-748-2003
25	896.5	55.3	237	10	US-09-880-748-2017
26	896.5	55.3	237	10	US-09-880-748-2019
27	896.5	55.3	237	10	US-09-880-748-2028
28	896.5	55.3	237	10	US-09-880-748-2110
29	896.5	55.3	237	12	US-10-293-418-2003
30	896.5	55.3	237	12	US-10-293-418-2017
31	896.5	55.3	237	12	US-10-293-418-2019
32	896.5	55.3	237	12	US-10-293-418-2028
33	896.5	55.3	237	12	US-10-293-418-2110
34	895.5	55.2	237	10	US-09-880-748-1906
35	895.5	55.2	237	12	US-10-293-418-1906
36	894.5	55.1	237	10	US-09-880-748-2040
37	894.5	55.1	237	12	US-10-293-418-2040
38	894	55.1	240	9	US-09-192-854-2
39	894	55.1	240	9	US-09-968-561A-2
40	894	55.1	240	10	US-09-968-744A-2
41	894	55.1	240	12	US-09-968-561A-2
42	894	55.1	248	10	US-09-880-748-1421
43	894	55.1	248	12	US-10-293-418-1421
44	889.5	54.8	237	10	US-09-880-748-2043
45	889.5	54.8	237	12	US-10-293-418-2043

ALIGNMENTS

RESULT 1
US-10-406-830-10
; Sequence 10, Application US/10406830
; Publication No. US20040071696A1
; GENERAL INFORMATION:
; APPLICANT: ADAMS, GREGORY P.
; APPLICANT: HORAK, EVA M.
; APPLICANT: WEINER, LOUIS M.
; TITLE OF INVENTION: BISPECIFIC SINGLE CHAIN Fv ANTIBODY MOLECULES AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 407T-000410US
; CURRENT APPLICATION NUMBER: US/10/406,830
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US 60/370,276
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic antibody.
US-10-406-830-10

Query Match 59.1%; Score 959; DB 12; Length 291;
Best Local Similarity 70.1%; Pred. No. 1.8e-60;
Matches 185; Conservative 31; Mismatches 38; Indels 10; Gaps 2;
QY 1 MAEVLQESGGGLVPGGSRKLSCAASGFTFSSFCMHVVRQAPKGLWYVYSSGSTI 60
DB 21 MAQVLQESGGGMVQPGKSLSLSCASGFTFSSYAMSVMVRQAPKGLWYSAISGSGST 80
QY 61 YYATVTKGRFTISRDNPNTLFLQWTSLSRSDTVMYICARD-----YGATVWGQGT 111
DB 81 YYADSVKGRFTISRDNSKNTLYLQNSLRADDTALTYCAREGYSNNWNWYFDLWGRGTL 140

;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; NUMBER OF SEQ ID NOS: 3239
;; SOFTWARE: Patent in Ver. 2.0
;; SEQ ID NO 2005
;; LENGTH: 237
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-880-748-2005

Query Match 55.5%; Score 900.5; DB 10; Length 237;
Best Local Similarity 72.2%; Pred. No. 2.1e-56;
Matches 171; Conservative 28; Mismatches 37; Indels 1; Gaps 1;

Qy 3 EVKLOESGGGLVQPGGSRKLSCAASGFTFSFGMHWVROAPEKGLEWVAYISSGSTIYY 62
Db 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFSYENWVRQAPGKLEWVSISSGSTIYY 60

Qy 63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYCYCARDYGYWGQGTITVTVSSGGSGG 122
Db 61 ADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYICARDTDDYWGQGTITVTVSSGGSGG 120

Qy 123 GGGSGGGSDIELTOSPAIMASGERVTMTCSASSV-RYMNWFOOKSGTSPKRWIYDT 181
Db 121 GGGSGGGSDIVMTQSPSTLSASVGDRTITCRASQGISLAWYQKPGKAPKVLIIKA 180

Qy 182 SKLSSGVPARFSGSGGTYSLTISSEAEADAATYCCQWSSNPLTFGAGTKLEIKR 238
Db 181 STLESQVSRFSGSGGTDFTLITISLQPEDFATYYCQSYSTPTWTFQGKLEIKR 237

RESULT 11
US-09-880-748-2114
; Sequence 2114, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 2114
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2114

Query Match 55.5%; Score 900.5; DB 10; Length 237;
Best Local Similarity 72.2%; Pred. No. 2.1e-56;
Matches 171; Conservative 28; Mismatches 37; Indels 1; Gaps 1;

Qy 3 EVKLOESGGGLVQPGGSRKLSCAASGFTFSFGMHWVROAPEKGLEWVAYISSGSTIYY 62
Db 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFSYENWVRQAPGKLEWVSISSGSTIYY 60

;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; NUMBER OF SEQ ID NOS: 3239
;; SOFTWARE: Patent in Ver. 2.0
;; SEQ ID NO 2005
;; LENGTH: 237
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-880-748-2005

Query Match 55.5%; Score 900.5; DB 10; Length 237;
Best Local Similarity 72.2%; Pred. No. 2.1e-56;
Matches 171; Conservative 28; Mismatches 37; Indels 1; Gaps 1;

Qy 3 EVKLOESGGGLVQPGGSRKLSCAASGFTFSFGMHWVROAPEKGLEWVAYISSGSTIYY 62
Db 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFSYENWVRQAPGKLEWVSISSGSTIYY 60

Qy 63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYCYCARDYGYWGQGTITVTVSSGGSGG 122
Db 61 ADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYICARDTDDYWGQGTITVTVSSGGSGG 120

Qy 123 GGGSGGGSDIELTOSPAIMASGERVTMTCSASSV-RYMNWFOOKSGTSPKRWIYDT 181
Db 121 GGGSGGGSDIVMTQSPSTLSASVGDRTITCRASQGISLAWYQKPGKAPKVLIIKA 180

Qy 182 SKLSSGVPARFSGSGGTYSLTISSEAEADAATYCCQWSSNPLTFGAGTKLEIKR 238
Db 181 STLESQVSRFSGSGGTDFTLITISLQPEDFATYYCQSYSTPTWTFQGKLEIKR 237

RESULT 12
US-10-293-418-2005
; Sequence 2005, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2005
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-2005

Query Match 55.5%; Score 900.5; DB 12; Length 237;
Best Local Similarity 72.2%; Pred. No. 2.1e-56;
Matches 171; Conservative 28; Mismatches 37; Indels 1; Gaps 1;

Qy 3 EVKLOESGGGLVQPGGSRKLSCAASGFTFSFGMHWVROAPEKGLEWVAYISSGSTIYY 62
Db 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFSYENWVRQAPGKLEWVSISSGSTIYY 60

Qy 63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYCYCARDYGYWGQGTITVTVSSGGSGG 122
Db 61 ADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYICARDTDDYWGQGTITVTVSSGGSGG 120

Qy 123 GGGSGGGSDIELTOSPAIMASGERVTMTCSASSV-RYMNWFOOKSGTSPKRWIYDT 181
Db 121 GGGSGGGSDIVMTQSPSTLSASVGDRTITCRASQGISLAWYQKPGKAPKVLIIKA 180

Qy 182 SKLSSGVPARFSGSGGTYSLTISSEAEADAATYCCQWSSNPLTFGAGTKLEIKR 238
Db 181 STLESQVSRFSGSGGTDFTLITISLQPEDFATYYCQSYSTPTWTFQGKLEIKR 237

RESULT 13
US-10-293-418-2114
; Sequence 2114, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2114
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-2114

Query Match 55.5%; Score 900.5; DB 12; Length 237;
Best Local Similarity 72.2%; Pred. No. 2.1e-56;
Matches 171; Conservative 28; Mismatches 37; Indels 1; Gaps 1;
QY 3 EVKLQESGGGLVOPGGSRKLSCAASGFTFSSFGMHVWROAPEKGLEWVAYISSGSTIYY 62
Db 1 QVQLVQSGGGLVOPGGSRKLSCAASGFTFSSYEMWVROAPGKLEWVSISSGSTIYY 60
QY 63 ADTVKGRFTISRDNPNKNTLFLQMTSLRSEDVVMYICARDYGAYWGQGTITVTVSSGGGGSG 122
Db 61 ADSVKGRFTISRDNKNSLYLQNSLRSEDVAVYICARDTTDYWGQGTITVTVSSGGGGSG 120
QY 123 GGGSGGGSDIELTQSPAIMSASPGERVMTCSASSV-RYMNWFOQKSGTSPKRWIYDT 181
Db 121 GGGSGGGSDIVMTQSPSTLSASVGRVITTCRASQGISLWLVYQKFGRAPKVLIYKA 180
QY 182 SKLSSGVPARFSGSGSGTSYSLTISSEAEADAATYCCQWSSNPLTFGAGTKLEIKR 238
Db 181 STLESQVPSRFRSGSGSGTDTLTITISLQPEDFATYCCQSYSTPWTFCGQTKLEIKR 237

RESULT 14
US-09-880-748-2118
; Sequence 2118, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 2118
; LENGTH: 237
; TYPE: PRT

; ORGANISM: Homo sapiens
US-09-880-748-2118
Query Match 55.5%; Score 899.5; DB 10; Length 237;
Best Local Similarity 72.2%; Pred. No. 2.5e-56;
Matches 171; Conservative 28; Mismatches 37; Indels 1; Gaps 1;
QY 3 EVKLQESGGGLVOPGGSRKLSCAASGFTFSSFGMHVWROAPEKGLEWVAYISSGSTIYY 62
Db 1 QVQLVQSGGGLVOPGGSRKLSCAASGFTFSSYEMWVROAPGKLEWVSISSGSTIYY 60
QY 63 ADTVKGRFTISRDNPNKNTLFLQMTSLRSEDVVMYICARDYGAYWGQGTITVTVSSGGGGSG 122
Db 61 ADSVKGRFTISRDNKNSLYLQNSLRSEDVAVYICARDTTDYWGQGTITVTVSSGGGGSG 120
QY 123 GGGSGGGSDIELTQSPAIMSASPGERVMTCSASSV-RYMNWFOQKSGTSPKRWIYDT 181
Db 121 GGGSGGGSDIVMTQSPSTLSASVGRVITTCRASQGISLWLVYQKFGRAPKVLIYKA 180
QY 182 SKLSSGVPARFSGSGSGTSYSLTISSEAEADAATYCCQWSSNPLTFGAGTKLEIKR 238
Db 181 STLESQVPSRFRSGSGSGTDTLTITISLQPEDFATYCCQSYSTPWTFCGQTKLEIKR 237

RESULT 15
US-10-293-418-2118
; Sequence 2118, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2118
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-2118

Query Match 55.5%; Score 899.5; DB 12; Length 237;
Best Local Similarity 72.2%; Pred. No. 2.5e-56;
Matches 171; Conservative 28; Mismatches 37; Indels 1; Gaps 1;
QY 3 EVKLQESGGGLVOPGGSRKLSCAASGFTFSSFGMHVWROAPEKGLEWVAYISSGSTIYY 62
Db 1 QVQLVQSGGGLVOPGGSRKLSCAASGFTFSSYEMWVROAPGKLEWVSISSGSTIYY 60
QY 63 ADTVKGRFTISRDNPNKNTLFLQMTSLRSEDVVMYICARDYGAYWGQGTITVTVSSGGGGSG 122
Db 61 ADSVKGRFTISRDNKNSLYLQNSLRSEDVAVYICARDTTDYWGQGTITVTVSSGGGGSG 120
QY 123 GGGSGGGSDIELTQSPAIMSASPGERVMTCSASSV-RYMNWFOQKSGTSPKRWIYDT 181
Db 121 GGGSGGGSDIVMTQSPSTLSASVGRVITTCRASQGISLWLVYQKFGRAPKVLIYKA 180

Oy 182 SKLSSGVPARFSGSGTSLTSSMEADATYCCOWSSNPLTFGAGTKLELKR 238
Db 181 STLESGVPSRPSGSGTDFTLTISSLOPEDFATYCCQSYSTWTFGQTKLEIKR 237

Search completed: May 27, 2004, 06:16:21
Job time : 758 secs